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OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 18:37:58 ; Search time 3870.2 Seconds  
(without alignments)  
11838.012 Million cell updates/sec

Title: US-09-378-759-10  
Perfect score: 2962  
Sequence: 1 CTCGTCGCCCGCGTGAAGA.....CCAGCCCCGCCCTCTGC 2962

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
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11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rnd:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
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54: gb\_sts2:\*  
55: gb\_sts3:\*  
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57: gb\_un:\*  
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98: em\_ba3:\*

pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
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| 1          | 2962  | 100.0       | 2962   | 9 AR084933  | AR084933 Sequence  |
| 2          | 2962  | 100.0       | 2962   | 9 AR084949  | AR084949 Sequence  |
| 3          | 2911  | 98.3        | 2962   | 97 HUMRPTKA | L36643 Homo sapien |
| 4          | 2233  | 75.4        | 3949   | 9 AX034855  | AX034855 Sequence  |
| 5          | 2233  | 75.4        | 3949   | 88 AF025304 | AF025304 Homo sapi |
| 6          | 1996  | 67.4        | 3768   | 9 AX034853  | AX034853 Sequence  |
| 7          | 1996  | 67.4        | 3768   | 9 HUMDRT    | L41939 Homo sapien |
| 8          | 1673  | 56.5        | 3151   | 97 HUMERKA  | D31661 Human mRNA  |



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OY 1201 ACTGACAGAGCCCTTCTCCCTCAGTTCGCTCTGTGAACATCACCACCACAGGCA 1260
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DB 1201 ACTGACAGAGCCCTTCTCCCTCAGTTCGCTCTGTGAACATCACCACCACAGGCA 1260
OY 1261 GCTCCATCGGAGTGTCCATCATGCATAGGTAGAGCCGACCCGTGGACAGCATTAACCTG 1320
    |||||||
DB 1261 GCTCCATCGGAGTGTCCATCATGCATAGGTAGAGCCGACCCGTGGACAGCATTAACCTG 1320
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    |||||||
DB 1321 TCGTGTCCTCCAGCCCGGACCCCAATGGCGTGAATCCTGGAGCTATGAGCTGAGACTAT 1380
OY 1381 GAGAGAGAGCTCAGTAGTACAAACGCCACAGCCATMAAAGCCGCCACCAAGACGGTCAAG 1440
    |||||||
DB 1381 GAGAGAGAGCTCAGTAGTACAAACGCCACAGCCATMAAAGCCGCCACCAAGACGGTCAAG 1440
OY 1441 GGCCTCAAAAGCCGGCCCATCTATGTCTTCCAGGTGGGGGACAGCATGTGGCAGAGCTAC 1500
    |||||||
DB 1441 GGCCTCAAAAGCCGGCCCATCTATGTCTTCCAGGTGGGGGACAGCATGTGGCAGAGCTAC 1500
OY 1501 GGGGCTCAGGAGGAGATGACTTCCAGACCATGACAGAAAGCCGAGTACAGCAAGC 1560
    |||||||
DB 1501 GGGGCTCAGGAGGAGATGACTTCCAGACCATGACAGAAAGCCGAGTACAGCAAGC 1560
OY 1561 ATCCAGAGAAAGTTCGCACTCATTCGGCTTCGCGCCGCTGGCCTGGCTTCTCTCAT 1620
    |||||||
DB 1561 ATCCAGAGAAAGTTCGCACTCATTCGGCTTCGCGCCGCTGGCCTGGCTTCTCTCAT 1620
OY 1621 GCTGTGTGTGTATCGCCATCGTGTGTGAACAGACGGGGTTTGACGCTGTCACTCGGAG 1680
    |||||||
DB 1621 GCTGTGTGTGTATCGCCATCGTGTGTGAACAGACGGGGTTTGACGCTGTCACTCGGAG 1680
OY 1681 TACAGGAGCAAGCTGCAACACTACACAGTGGCCACATTAACCCAGGAGTGAAGTCTAC 1740
    |||||||
DB 1681 TACAGGAGCAAGCTGCAACACTACACAGTGGCCACATTAACCCAGGAGTGAAGTCTAC 1740
OY 1741 ATCGATCCTTTACCTACGAGAGAGCCCAAGAGAGAGTGGGAGTTTGGCAAGAAAT 1800
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DB 1741 ATCGATCCTTTACCTACGAGAGAGCCCAAGAGAGAGTGGGAGTTTGGCAAGAAAT 1800
OY 1801 GACATCTCTGTGTCAAAATTTAGACAGTGTATCGGAGCGAGGGGAGTTTGGCAGGCTTC 1860
    |||||||
DB 1801 GACATCTCTGTGTCAAAATTTAGACAGTGTATCGGAGCGAGGGGAGTTTGGCAGGCTTC 1860
OY 1861 AGTGGCCACTGAAAGTGGCCAGGCAAGAGAGATCTTGTGGCCATCAAGAGCTCAAG 1920
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DB 1861 AGTGGCCACTGAAAGTGGCCAGGCAAGAGAGATCTTGTGGCCATCAAGAGCTCAAG 1920
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DB 1921 TCGGGCTACAGGAGAGAGAGCGCGGACTTCTGTAGGCAAGCCTTCATATGGGCCAG 1980
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DB 1981 TTGAGACATCCCAAGCTCATCCACCTGGAGGGTGTGTGTAACCAAGAGCACCCTGTGATG 2040
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DB 2041 ATCATCAGGAGTTCATGAGAGATGGCTCCTGTGAGTCTCTTCTCGGCAAAAAGATGGG 2100
OY 2101 CAGTTTCAAGTCACTCAGCTGTGGGCAATGCTTTCGGGGCATTCGACAGCTGGATGAATAC 2160
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DB 2101 CAGTTTCAAGTCACTCAGCTGTGGGCAATGCTTTCGGGGCATTCGACAGCTGGATGAATAC 2160
OY 2161 CTGGGAGACATGAATATGTTCACGCTGACCTGGCTGGCCGCAAACTCCGTCAACAGC 2220
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DB 2161 CTGGGAGACATGAATATGTTCACGCTGACCTGGCTGGCCGCAAACTCCGTCAACAGC 2220
OY 2221 AACCTGCTCAAGAGTGTGAGACTTGGGCTCTACAGCTTCTAGAGAGCATTAACCTCA 2280
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DB 2221 AACCTGCTCAAGAGTGTGAGACTTGGGCTCTACAGCTTCTAGAGAGCATTAACCTCA 2280

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OY 2281 GACCCCACTACACCACTGCCCTGGCGGAAAGTTTCCCATTCGGCTGGACAGCCCGGAA 2340
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DB 2281 GACCCCACTACACCACTGCCCTGGCGGAAAGTTTCCCATTCGGCTGGACAGCCCGGAA 2340
OY 2341 GCCATTCAGTACCGGAAGTTCACCTCGGCCAGTATGTGTGAGACTTGGCATTTGTATG 2400
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DB 2341 GCCATTCAGTACCGGAAGTTCACCTCGGCCAGTATGTGTGAGACTTGGCATTTGTATG 2400
OY 2401 TGGGAGTATGTCCTATGGGAGCGGCCCTTCTGAGACATGACCAACAGATGTAAATC 2460
    |||||||
DB 2401 TGGGAGTATGTCCTATGGGAGCGGCCCTTCTGAGACATGACCAACAGATGTAAATC 2460
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DB 2461 AATGCCATTGAGACAGACTATGCGCTGCACACCGCCCATGTGATCCCGAGCCCTGCAC 2520
OY 2521 CAACCTATGCTGAGACTGTGGGAGAGACCGCAACACCGGCGCCCAAGTTTGGCCAAAT 2580
    |||||||
DB 2521 CAACCTATGCTGAGACTGTGGGAGAGACCGCAACACCGGCGCCCAAGTTTGGCCAAAT 2580
OY 2581 GTCAACACGCTAGACAAAGATATCCGCAATCCAAACAGCTCAAAAGCCATGCGCCCTC 2640
    |||||||
DB 2581 GTCAACACGCTAGACAAAGATATCCGCAATCCAAACAGCTCAAAAGCCATGCGCCCTC 2640
OY 2641 TCTCTGGCATCAACCTGCGCTGTGGAGCGCAAGATCCCGACTACACGAGCTTAAAC 2700
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DB 2641 TCTCTGGCATCAACCTGCGCTGTGGAGCGCAAGATCCCGACTACACGAGCTTAAAC 2700
OY 2701 ACGGTGACAGATGTGGAGGAGCCATCAAGATGGGGAGTCAAGAGAGAGCTTGGCCAT 2760
    |||||||
DB 2701 ACGGTGACAGATGTGGAGGAGCCATCAAGATGGGGAGTCAAGAGAGAGCTTGGCCAT 2760
OY 2761 GCCGGCTTACCTCTTTGACGTGTGTCTAGATGATGAGAGACATTTCTCGGGTT 2820
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DB 2761 GCCGGCTTACCTCTTTGACGTGTGTCTAGATGATGAGAGACATTTCTCGGGTT 2820
OY 2821 GGGGTCACTTTGGCTGGGCGACAGAAAAAATCTGGAAGATATCCAGTATGCGGGCG 2880
    |||||||
DB 2821 GGGGTCACTTTGGCTGGGCGACAGAAAAAATCTGGAAGATATCCAGTATGCGGGCG 2880
OY 2881 CAGATGAACAGATTCAGTCTGTGGAGGTTTGACATTCACCTGCGCTCAGCTCTTC 2940
    |||||||
DB 2881 CAGATGAACAGATTCAGTCTGTGGAGGTTTGACATTCACCTGCGCTCAGCTCTTC 2940
OY 2941 CTCAAGCCCGGCCCTCTGTGC 2962
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DB 2941 CTCAAGCCCGGCCCTCTGTGC 2962

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RESULT 2  
 AR084949 2962 bp DNA PART 01-SEP-2000  
 LOCUS AR084949 Sequence 10 from patent US 5981246.  
 DEFINITION AR084949  
 ACCESSION AR084949  
 VERSION AR084949.1 GI:10011720  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2962)  
 AUTHORS Fox,G.M., Weicher,A.A. and Jing,S.  
 TITLE Nucleic acids encoding Eph-like receptor protein tyrosine kinases  
 JOURNAL Patent: US 5981246-A 10 09-NOV-1999;  
 FEATURES  
 source location/Qualifiers  
 1..2962  
 BASE COUNT 654 a 914 c 827 g 567 t  
 ORIGIN  
 Query Match 100.0%; Score 2962; DB 9; Length 2962;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|----|------|---|------|
| QY | 1    | CTGCTGCGCGCGTGGAAAGCAACGCTATGACTGACTACAGCGGACTGCTGAGCTGGGC    | 60   |
| Db | 1    | CTGCTCCCGCGCGTGGAAAGCAACGCTATGACTGACTACAGCGGACTGCTGAGCTGGGC   | 60   |
| QY | 61   | TGGATGGGATCCCTCCATCAGGGGTGGGAAGAGTGAATGGCTACGATGAAACATGAC     | 120  |
| Db | 61   | TGGATGGGATCCCTCCATCAGGGGTGGGAAGAGTGAATGGCTACGATGAAACATGAC     | 120  |
| QY | 121  | ACGATCCGACAGTACCAAGGTGTGCAAGCTGTTTGAATCAACCCAGAACCACTGGCTACGG | 180  |
| Db | 121  | ACGATCCGACAGTACCAAGGTGTGCAAGCTGTTTGAATCAACCCAGAACCACTGGCTACGG | 180  |
| QY | 181  | ACCAAGTTTATCCGGCGCGCTGGGGGCCACCGCATTCACGTGGAGATGAATTTTCGGTG   | 240  |
| Db | 181  | ACCAAGTTTATCCGGCGCGCTGGGGGCCACCGCATTCACGTGGAGATGAATTTTCGGTG   | 240  |
| QY | 241  | CGTAGCTGACAGCATCCCGAGGCTGCTGGCTCCGCAAGGAGACCTTCAACCTCTAT      | 300  |
| Db | 241  | CGTAGCTGACAGCATCCCGAGGCTGCTGGCTCCGCAAGGAGACCTTCAACCTCTAT      | 300  |
| QY | 301  | TACTATAGGCTGACTTTGACTCGGCACCAAGACCTTCCCAACCTGATGAGAAATCCA     | 360  |
| Db | 301  | TACTATAGGCTGACTTTGACTCGGCACCAAGACCTTCCCAACCTGATGAGAAATCCA     | 360  |
| QY | 361  | TGGGTGAAGGTGGATACCATTTGACACCGGAGAGAGCTTCTCCAGGTGGACTGGGTGC    | 420  |
| Db | 361  | TGGGTGAAGGTGGATACCATTTGACACCGGAGAGAGCTTCTCCAGGTGGACTGGGTGC    | 420  |
| QY | 421  | CGGCTATGAAATTCACACCGAGGTGGAGAGCTTGGAGCTGTGTCCGACGCGCTTC       | 480  |
| Db | 421  | CGGCTATGAAATTCACACCGAGGTGGAGAGCTTGGAGCTGTGTCCGACGCGCTTC       | 480  |
| QY | 481  | TACCTGGCTTCCAGAGACTATGGCGGCTGCATGTCTCTCATTCGCGCTGTCTTAC       | 540  |
| Db | 481  | TACCTGGCTTCCAGAGACTATGGCGGCTGCATGTCTCTCTCATTCGCGCTGTCTTAC     | 540  |
| QY | 541  | CGCAATGCCCCCGCATCATCCAGAAATGGGCGCATCTTCAGGAAACCTGTGGGGGCT     | 600  |
| Db | 541  | CGCAATGCCCCCGCATCATCCAGAAATGGGCGCATCTTCAGGAAACCTGTGGGGGCT     | 600  |
| QY | 601  | GAGAGACATGCTGTGGTGGCTCCCGGGGAGCTGCATCGCAATGCGGAAGAGTGGAT      | 660  |
| Db | 601  | GAGAGACATGCTGTGGTGGCTCCCGGGGAGCTGCATCGCAATGCGGAAGAGTGGAT      | 660  |
| QY | 661  | GTAACCATTAAGCTTACGTACGAGGAGGAGGAGGAGTGGTGGTCCCATCGGGGCTGC     | 720  |
| Db | 661  | GTAACCATTAAGCTTACGTACGAGGAGGAGGAGGAGTGGTGGTCCCATCGGGGCTGC     | 720  |
| QY | 721  | ATGTGCAAAAGCAGGCTTCGAGGCGGTTGAGAAATGGCACGCTGTCCGAGGTTGTCCATCT | 780  |
| Db | 721  | ATGTGCAAAAGCAGGCTTCGAGGCGGTTGAGAAATGGCACGCTGTCCGAGGTTGTCCATCT | 780  |
| QY | 781  | GGGACTTTCAAGGCGCAACCAAGGGGATGAGGCTGTACCCACTGTCCCATCAACGCGG    | 840  |
| Db | 781  | GGGACTTTCAAGGCGCAACCAAGGGGATGAGGCTGTACCCACTGTCCCATCAACGCGG    | 840  |
| QY | 841  | ACCACTTCTGAAGGGCGCAACCACTGTGTGCGCAATGGCTACTACAGAGAGACCTG      | 900  |
| Db | 841  | ACCACTTCTGAAGGGCGCAACCACTGTGTGCGCAATGGCTACTACAGAGAGACCTG      | 900  |
| QY | 901  | GACCCCTGGACATGCGCTGCAACCAACCATCCCTCCGCGCGCCAGGCTGTGATTTCCAGT  | 960  |
| Db | 901  | GACCCCTGGACATGCGCTGCAACCAACCATCCCTCCGCGCGCCAGGCTGTGATTTCCAGT  | 960  |
| QY | 961  | GTTCATGAGACCTCCCTCATGTGTGGAGTGAACCCCTCCCGGACTTCGGAAGCCGAGAG   | 1020 |
| Db | 961  | GTTCATGAGACCTCCCTCATGTGTGGAGTGAACCCCTCCCGGACTTCGGAAGCCGAGAG   | 1020 |
| QY | 1021 | GACCTGCTTACACATCATCTGCAAGAGCTGTGGCTGGGGCGGGGTGCTGCAACCCGCG    | 1080 |
| Db | 1021 | GACCTGCTTACACATCATCTGCAAGAGCTGTGGCTGGGGCGGGGTGCTGCAACCCGCG    | 1080 |
| QY | 1081 | TGGGGGGAACATGTACAGTACGACACGACGCTAGGCTGTACGAGCAACGATTTAC       | 1140 |
| Db | 1081 | TGGGGGGAACATGTACAGTACGACACGACGCTAGGCTGTACGAGCAACGATTTAC       | 1140 |
| QY | 1141 | ATCAGTCACTGTGTGGCCACACCGCATGACACTTTCGAGATCCAGGCTGTGAAGCGGCTT  | 1200 |
| Db | 1141 | ATCAGTCACTGTGTGGCCACACCGCATGACACTTTCGAGATCCAGGCTGTGAAGCGGCTT  | 1200 |
| QY | 1201 | ACTGACGAGACCCCTTTCGCTCAGTGTGGCTGTGTGAACATCACCACCAACGAGCA      | 1260 |
| Db | 1201 | ACTGACGAGACCCCTTTCGCTCAGTGTGGCTGTGTGAACATCACCACCAACGAGCA      | 1260 |
| QY | 1261 | GCTCCATCGGAGTATCCATCATCAGGTGAGGCGCACCGTAGAGATTAACCTG          | 1320 |
| Db | 1261 | GCTCCATCGGAGTATCCATCATCAGGTGAGGCGCACCGTAGAGATTAACCTG          | 1320 |
| QY | 1321 | TGCTGTCCCGCGCGGACACCCCAATGGGCTGATCCTTGGACTATGAGCTCAGTACTAT    | 1380 |
| Db | 1321 | TGCTGTCCCGCGCGGACACCCCAATGGGCTGATCCTTGGACTATGAGCTCAGTACTAT    | 1380 |
| QY | 1381 | GAGAAGAGCTCATGTAGATACAAAGCCACACGCTTAAATAACCCACCAACAGGCTACAG   | 1440 |
| Db | 1381 | GAGAAGAGCTCATGTAGATACAAAGCCACACGCTTAAATAACCCACCAACAGGCTACAG   | 1440 |
| QY | 1441 | GGCTCAAAGCGGCGCATCTATGTCTTCCAGGTGGCGGACGACTGTGGAGGCTAC        | 1500 |
| Db | 1441 | GGCTCAAAGCGGCGCATCTATGTCTTCCAGGTGGCGGACGACTGTGGAGGCTAC        | 1500 |
| QY | 1501 | GGGGCTACAGCGGCAAGATGATCTTCCAGACCATGACAGAAAGCGGAGTCCACAAAGC    | 1560 |
| Db | 1501 | GGGGCTACAGCGGCAAGATGATCTTCCAGACCATGACAGAAAGCGGAGTCCACAAAGC    | 1560 |
| QY | 1561 | ATCCAGAGAAATTTGCCATCATCATGAGGCTCTCGGCGCGCTGGCTGTCTTCATTT      | 1620 |
| Db | 1561 | ATCCAGAGAAATTTGCCATCATCATGAGGCTCTCGGCGCGCTGGCTGTCTTCATTT      | 1620 |
| QY | 1621 | GCTGTGGTGTGCATGCGCATCTGTGTGTAAAGAGAGGGGGTTTGAAGCTGTGATCCGAG   | 1680 |
| Db | 1621 | GCTGTGGTGTGCATGCGCATCTGTGTGTAAAGAGAGGGGGTTTGAAGCTGTGATCCGAG   | 1680 |
| QY | 1681 | TACACGACAAGCTGCAACACTACACCAAGTGGCCATTAACCCGACGATGAAGATCTAC    | 1740 |
| Db | 1681 | TACACGACAAGCTGCAACACTACACCAAGTGGCCATTAACCCGACGATGAAGATCTAC    | 1740 |
| QY | 1741 | ATGATATCTTTACCTTACGAGAGACCCCAAGGAGCAATGCGGGAGTTTGCACAAAGAAAT  | 1800 |
| Db | 1741 | ATGATATCTTTACCTTACGAGAGACCCCAAGGAGCAATGCGGGAGTTTGCACAAAGAAAT  | 1800 |
| QY | 1801 | GACATCTCTGTGTCAAAATTTGAGCAGGTGATGGACACAGGGGATTTGGCGAGGTGTC    | 1860 |
| Db | 1801 | GACATCTCTGTGTCAAAATTTGAGCAGGTGATGGACACAGGGGATTTGGCGAGGTGTC    | 1860 |
| QY | 1861 | AGTGGCACCTGGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCATCAAGAGCTTCAG      | 1920 |
| Db | 1861 | AGTGGCACCTGGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCATCAAGAGCTTCAG      | 1920 |
| QY | 1921 | TGGGGCTTACACGGAAGAGCGCGCGGAGCTTCTCTGAGCAAGCTTCATCATGAGGCGAG   | 1980 |
| Db |      |   |      |



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|||||
Db 2161 CTGGAGACAGAACTATGTTACCGTGACCTGCTGCCGCAACATCTCTGCAACAGC 2220
|||
Qy 2221 AACCTGATCTGCAAGTGTGCGAGCTTTGGGCTCTACGCTTTCTAGAGAGATACCTCA 2280
|||||
Db 2221 AACCTGATCTGCAAGTGTGCGAGCTTTGGGCTCTACGCTTTCTAGAGAGATACCTCA 2280
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Qy 2281 GACCCACCTACACAGAGTGGCCCTGGCGGAAAGTTCCCATCTCCCTGACAGCCCCGGAA 2340
2281 GACCCACCTACACAGAGTGGCCCTGGCGGAAAGTTCCCATCTCCCTGACAGCCCCGGAA 2340
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Qy 2341 GCCATCCGATCCGGAATGACCTCGGCGCATGATGTGTGAGAGTACGCGCATTTGCAATG 2400
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Db 2341 GCCATCCGATCCGGAATGACCTCGGCGCATGATGTGTGAGAGTACGCGCATTTGCAATG 2400
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Qy 2401 TGGAGAGTGTGCTCTATGAGGAGCGCCCTTACTGGAACATGACCAACAGATGTATC 2460
2401 TGGAGAGTGTGCTCTATGAGGAGCGCCCTTACTGGAACATGACCAACAGATGTATC 2460
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2461 AATGCCATTGACAGAGATCTATGGGCTGCCACCGCCCATGAGACTGCGCGAGCCCTGAC 2520
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Qy 2521 CAACATATGCTGAGCTGTTGGCAGAGACCGCAACACCGCGCCCAAGTTGCGCCAAAT 2580
2521 CAACATATGCTGAGCTGTTGGCAGAGACCGCAACACCGCGCCCAAGTTGCGCCAAAT 2580
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2581 GTCACACGCTAGACAAAGATGATCCGCAATCCCAACAGCTTAAAGCCCTGCGCCCTC 2640
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2641 TCTCTGCGATCAACCTGCCCGCTGCTGGACCGGACGATCCCGACCTACACAGCTTAA 2700
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Db 2641 TCTCTGCGATCAACCTGCCCGCTGCTGGACCGGACGATCCCGACCTACACAGCTTAA 2700
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2821 GGGGTCACTTGGCTGGCCACGAGAAAAATCTGTAACAGTATCCAGTGTATGCGGGC 2880
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Db 2881 CAGATGAACAGATTCAGTCTGTGAGAGTTTGACATTCACCTGCTGCTCATTTC 2940
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Qy 2941 CTCGAAGCCCCCCCCCTCTGC 2962
2941 CTCGAAGCCCCCCCCCTCTGC 2962
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Db 2941 CTCGAAGCCCCCCCCCTCTGC 2962
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## RESULT 3

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LOCUS HUMRPTKA 2962 bp mRNA PRI 10-AUG-1995
DEFINITION Homo sapiens receptor protein-tyrosine kinase (HEK5) mRNA, 3' end.
ACCESSION L36643
VERSION L36643.1 GI:551609
KEYWORDS EPH-like receptor PTK; receptor protein-tyrosine kinase.
SOURCE Homo sapiens (clone library: Stratagene premade library, cat #936206) female fetus, 17-18 weeks gestation brain cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2962)
AUTHORS Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M.,
Baeu,R. and Welcher,A.A.
TITLE cDNA cloning and tissue distribution of five human EPH-like
receptor protein-tyrosine kinases

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JOURNAL Oncogene 10 (5), 897-905 (1995)
MEDLINE 95206782
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ORIGIN
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| OY | 421  | CGCGTCATGAAAATCAACACCGAGGTGCGGAGCTTCGGACCTGTGTGCCGACGGCGCTTC        | 480  |
| Db | 421  | CGCGTCATGAAAATCAACACCGAGGTGCGGAGCTTCGGACCTGTGTGCCGACGGCGCTTC        | 480  |
| OY | 481  | TACCTGGGCTTCCAGAGACTATGGCGGGCTGCATCTCCCTCATTCGCCGTGCTGTCTTAC        | 540  |
| Db | 481  | TACCTGGGCTTCCAGAGACTATGGCGGGCTGCATCTCCCTCATTCGCCGTGCTGTCTTAC        | 540  |
| OY | 541  | CGCAAGTCCCCCGCATCATCCAGAAATGGCGGCATCTTCCAGSAAACCTGTGGGGGCT          | 600  |
| Db | 541  | CGCAAGTCCCCCGCATCATCCAGAAATGGCGGCATCTTCCAGSAAACCTGTGGGGGCT          | 600  |
| OY | 601  | GAGAGCAATCGCTGGGTGGGTGCCGGGGGACACTGCATCGCAATGCGSAGAGGTGGAT          | 660  |
| Db | 601  | GAGAGCAATCGCTGGGTGGGTGCCGGGGGACACTGCATCGCAATGCGSAGAGGTGGAT          | 660  |
| OY | 661  | GTACCCATCAAGCTTACTGTATACGGGGGACGGCAGTGGTGGTCCCATCGGGGCTGC           | 720  |
| Db | 661  | GTACCCATCAAGCTTACTGTATACGGGGGACGGCAGTGGTGGTCCCATCGGGGCTGC           | 720  |
| OY | 721  | ATGCGAAACAGGCTTCAGGCGCTTGAGAAATGGCAACCGCTGCCAGGTGTTCATCT            | 780  |
| Db | 721  | ATGCGAAACAGGCTTCAGGCGCTTGAGAAATGGCAACCGCTGCCAGGTGTTCATCT            | 780  |
| OY | 781  | GGGACTTTCAAAGCCCAACCAAGGGGATGAGGCTGTGCCGAAATGGCTACTTACAGAGACCTG     | 840  |
| Db | 781  | GGGACTTTCAAAGCCCAACCAAGGGGATGAGGCTGTGCCGAAATGGCTACTTACAGAGACCTG     | 840  |
| OY | 841  | ACCACCTTGAAGGGGGCCCAACGACTGTCTGTCCGCAATGGCTACTTACAGAGACCTG          | 900  |
| Db | 841  | ACCACCTTGAAGGGGGCCCAACGACTGTCTGTCCGCAATGGCTACTTACAGAGACCTG          | 900  |
| OY | 901  | GACCCCTTGAGACATGCGCTGCAACACATCCCTCCGCGCCAGGCTGTGAATTCAGT            | 960  |
| Db | 901  | GACCCCTTGAGACATGCGCTGCAACACATCCCTCCGCGCCAGGCTGTGAATTCAGT            | 960  |
| OY | 961  | GTCAAATGAGACCTCCCTCATCTGTGAATGGACCCCTCCCGCGACTCCGAGGCCGAGAG         | 1020 |
| Db | 961  | GTCAAATGAGACCTCCCTCATCTGTGAATGGACCCCTCCCGCGACTCCGAGGCCGAGAG         | 1020 |
| OY | 1021 | GACCTGTGTACACATCATCTGGAAGGCGTGGGCTCGGGGCGGGGTGCTGCACCCGC            | 1080 |
| Db | 1021 | GACCTGTGTACACATCATCTGGAAGGCGTGGGCTCGGGGCGGGGTGCTGCACCCGC            | 1080 |
| OY | 1081 | TGGGGGGACATGTACGACTACGCACACGCCGAGCTAGGGCTACACGAGGCACGCAATTAC        | 1140 |
| Db | 1081 | TGGGGGGACATGTACGACTACGCACACGCCGAGCTAGGGCTACACGAGGCACGCAATTAC        | 1140 |
| OY | 1141 | ATCAGTGAACCTGTGAGGCCACACCAACCAATACACTTGSAAATCAGAGCTGTGAAGGGCTT      | 1200 |
| Db | 1141 | ATCAGTGAACCTGTGAGGCCACACCAACCAATACACTTGSAAATCAGAGCTGTGAAGGGCTT      | 1200 |
| OY | 1201 | ACTGACCAAGACCCCTTCTGCGCTCAGATTCCGCTGTGTGAACATACCAACCAAGGCA          | 1260 |
| Db | 1201 | ACTGACCAAGACCCCTTCTGCGCTCAGATTCCGCTGTGTGAACATACCAACCAAGGCA          | 1260 |
| OY | 1261 | GCTTCATGGGAGGTGCATCATATGCAATGCAATGAGCGGACCGACCTGTGAGCACTTACCTGT     | 1320 |
| Db | 1261 | GCTTCATGGGAGGTGCATCATATGCAATGCAATGAGCGGACCGACCGACCTGTGAGCACTTACCTGT | 1320 |
| OY | 1321 | TGCTGTGCTCCAGCGCGGACACGCCCAATGGCTGTGATCTGTGACTATGAGCTGTCAATTAAT     | 1380 |
| Db | 1321 | TGCTGTGCTCCAGCGCGGACACGCCCAATGGCTGTGATCTGTGACTATGAGCTGTCAATTAAT     | 1380 |
| OY | 1381 | GAGAAAGAGGTCAGTGTGATCAAAACGCGCACAGCCATAAAAAGCCCGACCAACAGCGTACAG     | 1440 |
| Db | 1381 | GAGAAAGAGGTCAGTGTGATCAAAACGCGCACAGCCATAAAAAGCCCGACCAACAGCGTACAG     | 1440 |
| OY | 1441 | GGGCTCAAAAGCCGGCCCATCATATGTCTTCCAGGTGTGGGGAGCGCACTGTGGAGGCTTAC      | 1500 |
| Db | 1441 | GGGCTCAAAAGCCGGCCCATCATATGTCTTCCAGGTGTGGGGAGCGCACTGTGGAGGCTTAC      | 1500 |

|    |      |   |      |
|----|------|---|------|
| QY | 1501 | GGGCGCTAACAGCGCCAGAGTGTACTTCCAGACCATTAGACAGAAAGCCGAGTACCAGCAAGC   | 1560 |
| Db | 1501 | GGGCGCTAACAGCGCCAGAGTGTACTTCCAGACCATTAGACAGAAAGCCGAGTACCAGCAAGC   | 1560 |
| QY | 1561 | ATCCAGGAGAACTTGGCACTCTCAATCGGCTCTCTGGCGCTGGCGTGGTCTTCTCTATT       | 1620 |
| Db | 1561 | ATCCAGGAGAACTTGGCACTCTCAATCGGCTCTCTGGCGCTGGCGTGGTCTTCTCTATT       | 1620 |
| QY | 1621 | GCTGTGGTGTTCATCCGCATCGTGTGTAAACAGACGGGGGTTTGAAGCTGTGCACTCGAG      | 1680 |
| Db | 1621 | GCTGTGGTGTTCATCCGCATCGTGTGTAAACAGACGGGGGTTTGAAGCTGTGCACTCGAG      | 1680 |
| QY | 1681 | TACACGGCAAGCTCTCAACACTCAACCCAGTGGCCCAATATACCAGCATAGAGATCTTAC      | 1740 |
| Db | 1681 | TACACGGCAAGCTCTCAACACTCAACCCAGTGGCCCAATATACCAGCATAGAGATCTTAC      | 1740 |
| QY | 1741 | ATCGATCTTTTCACCTTACGAGAGACCCCAACGAGGCACTGGGGAGTTTGGCAAGGAATT      | 1800 |
| Db | 1741 | ATCGATCTTTTCACCTTACGAGAGACCCCAACGAGGCACTGGGGAGTTTGGCAAGGAATT      | 1800 |
| QY | 1801 | GACATCTCTCTGTGTCGCAAAATTGACAGAGTATGCGACAGGGGAGTTTGGCGAGCTCTGC     | 1860 |
| Db | 1801 | GACATCTCTCTGTGTCGCAAAATTGACAGAGTATGCGACAGGGGAGTTTGGCGAGCTCTGC     | 1860 |
| QY | 1861 | AGTGGCCACTGTAAGCTGCCAGGCAAGAGAGACTTTTGTGGCCATCAAGACGCTCAAG        | 1920 |
| Db | 1861 | AGTGGCCACTGTAAGCTGCCAGGCAAGAGAGACTTTTGTGGCCATCAAGACGCTCAAG        | 1920 |
| QY | 1921 | TCGGGGCTAACGGGGAAGCAGCGCGGGGACTTCTCTAGCCAGACCTTCATCATGGGCCAG      | 1980 |
| Db | 1921 | TCGGGGCTAACGGGGAAGCAGCGCGGGGACTTCTCTAGCCAGACCTTCATCATGGGCCAG      | 1980 |
| QY | 1981 | TTGCAACCATCCCAACGTCATCCACCTTGGAGGGTGTGTGCCAAGAGCAGACCTGTGATG      | 2040 |
| Db | 1981 | TTGCAACCATCCCAACGTCATCCACCTTGGAGGGTGTGTGTACCAAGAGCAGACCTGTGATG    | 2040 |
| QY | 2041 | ATCATTCACGAGTTCAATGGAGAAATGGCTCCCTGGACTCTTCTCCGGCAAAACGATGGG      | 2100 |
| Db | 2041 | ATCATTCACGAGTTCAATGGAGAAATGGCTCCCTGGACTCTTCTCCGGCAAAACGATGGG      | 2100 |
| QY | 2101 | CAGTTTCACACTTCATCCAGCTGGTGGGCATATGCTTCGGGGGATGCGACGTGGGATGAAAGTAC | 2160 |
| Db | 2101 | CAGTTTCACACTTCATCCAGCTGGTGGGCATATGCTTCGGGGGATGCGACGTGGGATGAAAGTAC | 2160 |
| QY | 2161 | CTGGCAGACATGACATATATGTTTCAACGCTGACCTGGCTGCCCGCAACATCTCTGTCAAACAGC | 2220 |
| Db | 2161 | CTGGCAGACATGACATATATGTTTCAACGCTGACCTGGCTGCCCGCAACATCTCTGTCAAACAGC | 2220 |
| QY | 2221 | AACCTGTGTGCAAGTGTGTCGAGCTTTGGGGCTCTACAGCTTTCTAGAGAGCATATCTCA      | 2280 |
| Db | 2221 | AACCTGTGTGCAAGTGTGTCGAGCTTTGGGGCTCTCTACAGCTTTCTAGAGAGCATATCTCA    | 2280 |
| QY | 2281 | GACCCCACTACACAGTGCCTTGGGGGAAAGTTTCCCATCCGCTGACAGACCCCGGAA         | 2340 |
| Db | 2281 | GACCCCACTACACAGTGCCTTGGGGGAAAGTTTCCCATCCGCTGACAGACCCCGGAA         | 2340 |
| QY | 2341 | GGCATCTACTACCGAAGTTCACCTCCGCGCAAGTATGTGTGAGCTTACGGCATTTGTCATG     | 2400 |
| Db | 2341 | GGCATCTACTACCGAAGTTCACCTCCGCGCAAGTATGTGTGAGCTTACGGCATTTGTCATG     | 2400 |
| QY | 2401 | TGGGAGGTGATGTCCTATGGGGAGCGCCCTACTGAGCATATGACCAACAGAGATGTATC       | 2460 |
| Db | 2401 | TGGGAGGTGATGTCCTATGGGGAGCGCCCTACTGAGCATATGACCAACAGAGATGTATC       | 2460 |
| QY | 2461 | AATGCATTTGAGCAGACTATTCGGTGGCCACCGCCATGCACTGCCCGAGCGCCCTTGAC       | 2520 |
| Db | 2461 | AATGCATTTGAGCAGACTATTCGGTGGCCACCGCCATGCACTGCCCGAGCGCCCTTGAC       | 2520 |
| QY | 2521 | CAACTCATGCTGAGCTGTGGCAGAAAGACCGCAACACCGGCCCAAGTTTGGCGCAAAATT      | 2580 |
| Db | 2521 | CAACTCATGCTGAGCTGTGGCAGAAAGACCGCAACACCGGCCCAAGTTTGGCGCAAAATT      | 2580 |
| QY | 2581 | GTCACACGCTAGACAGAGATGATCCGAAATCCCAACGCTTCAAAGCATATGGCGCCCTTC      | 2640 |

|    |      |  |      |
|----|------|--|------|
| Db | 2581 | GTCAACACCGGTAAACAAAGATGATTCGGCAATCCCAACACCTCTCAAGCCATGCGCCCTTC     | 2640 |
| Qy | 2641 | TTCCCTTGGCATCTCAACCTGGCCGCTGGCTGGACCGCACAGATCCCGCATACACCAAGCTTTAAC | 2700 |
| Db | 2641 | TTCCCTTGGCATCAACTGGCCGCTGGCTGGACCGCACAGATCCCGCATACACCAAGCTTTAAC    | 2700 |
| Qy | 2701 | ACGGTGACACAGAGCGCTGGAGGCCATCAAGATGGGGCAGTACAAAGAGAGCTTGGCCAAAT     | 2760 |
| Db | 2701 | ACGGTGACACAGAGCGCTGGAGGCCATCAAGATGGGGCAGTACAAAGAGAGCTTGGCCAAAT     | 2760 |
| Qy | 2761 | GCCGGCTTTCACCTCTCTTGGACGTCGTCTCAGATGATGATGAGAGACATTTCTCCGGGTT      | 2820 |
| Db | 2761 | GCGGGCTTTCACCTCTTGGACGTCGTCTCAGATGATGATGAGAGACATTTCTCCGGGTT        | 2820 |
| Qy | 2821 | GGGGTCACTTTGGCTGGCCACCCAGAAAAAAATCTGTAACAGTATCCAGGTGATGGGGCG       | 2880 |
| Db | 2821 | GGGGTCACTTTGGCTGGCCACCCAGAAAAAAATCTGTAACAGTATCCAGGTGATGGGGCG       | 2880 |
| Qy | 2881 | CAGATGAACCAAGATTCAGTGTGTGGAGGTTTGAATTCACCTGACCTGGGCTACACTCTTC      | 2940 |
| Db | 2881 | CAGATGAACCAAGATTCAGTGTGTGGAGGTTTGAATTCACCTGACCTGGGCTACACTCTTC      | 2940 |
| Qy | 2941 | CTTCAAGCCCGGCCCTCTGCG  | 2962 |
| Db | 2941 | CTTCAAGCCCGGCCCTCTGCG  | 2962 |

[illegible]

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| Matches 2903          | Conservative | 0  |              |             |        |
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| Db                    | 68           | CTGTGCGCCCGCTGGAGAAACGCTAATGAGACTCACTACAGCGAGCTGTGAGCTGGCG     | 127          |             |        |
| OY                    | 61           | TGCAATGATGATCTCTCATCAGGCGTGGAGAGGATGCTGCTGAGTGAACATGAAC        | 120          |             |        |
| Db                    | 128          | TGCAATGATGATCTCTCATCAGGCGTGGAGAGGATGCTGCTGAGTGAACATGAAC        | 187          |             |        |
| OY                    | 121          | ACGATCCGCACAGTACAGAGGTGTGCAACGTGTTGATGATCAAGCCAGAACACTGGCTACGG | 180          |             |        |
| Db                    | 188          | ACGATCCGCACAGTACAGAGGTGTGCAACGTGTTGATGATCAAGCCAGAACACTGGCTACGG | 247          |             |        |
| OY                    | 181          | ACCAAGTTTATCCGGGGCGGTGGGGCCCAACCCATCCACGTGAGAGATGAATTTTCGGTG   | 240          |             |        |
| Db                    | 248          | ACCAAGTTTATCCGGGGCGGTGGGGCCCAACCCATCCACGTGAGAGATGAATTTTCGGTG   | 307          |             |        |
| OY                    | 241          | CGTAGCTGACAGACATCCCAACGCTGCTGGCTCTCTGACAGAGACCTTAAACCTTAT      | 300          |             |        |

|    |      |  |      |
|----|------|--|------|
| Db | 308  | CGTGACGACGACGATCCCGACGGCTGGCTGGCTCTGGACAAGGAGACCTTCAACCTCTAT   | 367  |
| Qy | 301  | TACTATGAGGCTGACTTTTGACTTCGGCCACCAAGACCTTCCCAACTGGATGGAAATCCA   | 360  |
| Db | 368  | TACTATGAGGCTGACTTTGACTTCGGCCACCAAGACCTTCCCAACTGGATGGAAATCCA    | 427  |
| Qy | 361  | TGGGTGAAGGTGGATACATTCGTACGCGGACGGAGACCTTCCAGGTGGACCTGGGTGGC    | 420  |
| Db | 428  | TGGGTGAAGGTGGATACATTCGTACGCGGACGGAGACCTTCCAGGTGGACCTGGGTGGC    | 487  |
| Qy | 421  | CGGCTCATGAAAAATCAACACCGAGGTGGAGCTTGGACCTGTGTCCGACGGCTTC        | 480  |
| Db | 488  | CGGCTCATGAAAAATCAACACCGAGGTGGAGCTTGGACCTGTGTCCGACGGCTTC        | 547  |
| Qy | 481  | TACCTGGCTTCCAGGACTATGGCGGCTGCATATGCCCATCGGCGGGTCTTCTAC         | 540  |
| Db | 548  | TACCTGGCTTCCAGGACTATGGCGGCTGCATATGCCCATCGGCGGGTCTTCTAC         | 607  |
| Qy | 541  | CGCAAGTCCCCCGCATATCCAGAAATGGCGCATCTTCCAGAAACCTGTGGGGGCT        | 600  |
| Db | 608  | CGCAAGTCCCCCGCATATCCAGAAATGGCGCATCTTCCAGAAACCTGTGGGGGCT        | 667  |
| Qy | 601  | GAGAGCAATCGCTGTGGTGGCTGCCGGGGCACTGCTATTCGCCATTCGGGAAAGATGGAT   | 660  |
| Db | 668  | GAGAGCAATCGCTGTGGTGGCTGCCGGGGCACTGCTATTCGCCATTCGGGAAAGATGGAT   | 727  |
| Qy | 661  | GTACCCATCAAGGCTCTGTATACGGGGAGCGGAGATGGAGTGTGCCATTCGGCGCTGC     | 720  |
| Db | 728  | GTACCCATCAAGGCTCTGTATACGGGGAGCGGAGATGGAGTGTGCCATTCGGCGCTGC     | 787  |
| Qy | 721  | ATGTGCAAAAGCAGGCTTGCAGGGCGTTGAGAAATGGCAACGCTGTGCCGAGTTTCTCATCT | 780  |
| Db | 788  | ATGTGCAAAAGCAGGCTTGCAGGGCGTTGAGAAATGGCAACGCTGTGCCGAGTTTCTCATCT | 847  |
| Qy | 781  | GGGACTTTCAGGGCAACCAAGGGGAAATGAGGCTGTACCACTATGCCATCAACAGCGG     | 840  |
| Db | 848  | GGGACTTTCAGGGCAACCAAGGGGAAATGAGGCTGTACCACTATGCCATCAACAGCGG     | 907  |
| Qy | 841  | ACCACCTTCTGAAGGGGACCACCAACTGTGTCGCCGAATGGCTACTACAGAGACAGCTG    | 900  |
| Db | 908  | ACCACCTTCTGAAGGGGACCACCAACTGTGTCGCCGAATGGCTACTACAGAGACAGCTG    | 967  |
| Qy | 901  | GACCCCTTGGACATGCGCTGACAAACATCCCTCGGGCGCCCAAGCTGTGATTTCCAGT     | 960  |
| Db | 968  | GACCCCTTGGACATGCGCTGACAAACATCCCTCGGGCGCCCAAGCTGTGATTTCCAGT     | 1027 |
| Qy | 961  | GATCAATGAGACCTCCCTCATCTGGAATGGAGACCTTCCCGGAGCTCCGAGGCCGAGAG    | 1020 |
| Db | 1028 | GTCATATGAACTCCCTCATCTGGAATGGAGACCTTCCCGGAGCTCCGAGGCCGAGAG      | 1087 |
| Qy | 1021 | GACCTGTCTACACATCATCTGCAAGAGCTGTGGCTCGGGCGGGGTGCTGCACCCCGC      | 1080 |
| Db | 1088 | GACCTGTCTACACATCATCTGCAAGAGCTGTGGCTCGGGCGGGGTGCTGCACCCCGC      | 1147 |
| Qy | 1081 | TGGGGGGAATATGTACATATACGACACAGCGAGTATAGCCTGACCGAGGACGCAATTTAC   | 1140 |
| Db | 1148 | TGGGGGGAATATGTACATATACGACACAGCGAGTATAGCCTGACCGAGGACGCAATTTAC   | 1207 |
| Qy | 1141 | ATCAGTGAACCTGCTGGCCACACACCAGTAGACCTTGGAGATCCAGGCTGTGAACGGCTT   | 1200 |
| Db | 1208 | ATCAGTGAACCTGCTGGCCACACACCAGTAGACCTTGGAGATCCAGGCTGTGAACGGCTT   | 1267 |
| Qy | 1201 | ACTGACCAAGGCCCTTCTCGCGCTCAGTGTGGCCCTGTGAAACATTCACCAACAGGCA     | 1260 |
| Db | 1268 | ACTGACCAAGGCCCTTCTCGCGCTCAGTGTGGCCCTGTGAAACATTCACCAACAGGCA     | 1327 |
| Qy | 1261 | GCTCATCTGGCAATGCTCATATGATGATAGGTGAGCGGCACCGTGGACAGCAATTAACCTG  | 1320 |
| Db | 1328 | GCTCATCTGGCAATGCTCATATGATGATAGGTGAGCGGCACCGTGGACAGCAATTAACCTG  | 1387 |
| Qy | 1321 | TGCTGTGCCAGCGGACGACGCCCAATGGCTGATCCTGGACATATAGGCTGGCAGTACAT    | 1380 |

|            |            |  |      |
|------------|------------|--|------|
| QY         | 2455       | GTAAATCAATGCATTGAGCAGAGACTATGCGCTGGCACCGCCATGAGCTGCCGAGGCC     | 2514 |
| Db         | 2528       | GTATCAATATGCATTGAGCAGAGACTATGCGCTGCCACCGCCATGAGCTGCCGAGGCC     | 2587 |
| QY         | 2515       | CTGCACCAACTCATCTGCTGACTGTTGGCAGAAAGACCGCAACACCGGCCCAAGTTCCGC   | 2574 |
| Db         | 2588       | CTGCACCAACTCATCTGACTGTTGGCAGAAAGACCGCAACACCGGCCCAAGTTCCGC      | 2647 |
| QY         | 2575       | CAAAATGTCAACACGCTGAGCAAGTGAATCCGCAATCCCAAGCCCTCAAGCCATATGGG    | 2634 |
| Db         | 2648       | CAAAATGTCAACACGCTGAGCAAGTGAATCCGCAATCCCAAGCCCTCAAGCCATATGGG    | 2707 |
| QY         | 2635       | CCCCTCTCTCTGGCATTCAACCTGCCGCTGCTGGACCGCAACGATCCCGACTACACACG    | 2694 |
| Db         | 2708       | CCCCTCTCTCTGGCATTCAACCTGCCGCTGCTGGACCGCAACGATCCCGACTACACACG    | 2767 |
| QY         | 2695       | TTTAAACAGGTTGGAGAGATGAGTGGCTGGAGGCAATCAAGTGGGGCAATGCAAGAGACTTC | 2754 |
| Db         | 2768       | TTTAAACAGGTTGGAGAGATGAGTGGCTGGAGGCAATCAAGTGGGGCAATGCAAGAGACTTC | 2827 |
| QY         | 2755       | GCCAAATGCCGGCTTCACTCTCTTTGAGAGTGTGTCTCAGATGATGATGAGAGCAATTCTC  | 2814 |
| Db         | 2828       | GCCAAATGCCGGCTTCACTCTCTTTGAGAGTGTGTCTCAGATGATGATGAGAGCAATTCTC  | 2887 |
| -QY        | 2815       | CGGGTTGGGGGTCACCTTTGGCTGGCCACACCAAAAAAATCTCTGACAGTATCCAGGTGATG | 2874 |
| Db         | 2888       | CGGGTTGGGGGTCACCTTTGGCTGGCCACACCAAAAAAATCTCTGACAGTATCCAGGTGATG | 2947 |
| QY         | 2875       | CGGGCGCAGATGAACAGATTTCACTGCTGTGGAG                             | 2908 |
| Db         | 2948       | CGGGCGCAGATGAACAGATTTCACTGCTGTGGAG                             | 2981 |
| RESULT     | 5          |  |      |
| LOCUS      | AF025304   |  |      |
| DEFINITION | AF025304   | 3949 bp  | MRNA |
| ACCESSION  | AF025304   |  |      |
| VERSION    | AF025304.1 | GI:2739055   |      |
| KEYWORDS   |            |  |      |
| SOURCE     |            |  |      |
| ORGANISM   |            |  |      |
| REFERENCE  |            |  |      |
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| Db | 608  | CGAAGTGGCCCCGCGATCATCCAGAAATGGCCCATCTTCCAGGAACCCGTGCGGGGGCT    | 667  |
| Qy | 601  | GAGAGCACTGCGTGGTGGCTGCCGGGGCAGCTGCATGCGCAATGGGAAAGGTGGAT       | 660  |
| Db | 668  | GAGAGCACTGCGTGGTGGCTGCCGGGGCAGCTGCATGCGCAATGGGAAAGGTGGAT       | 727  |
| Qy | 661  | GTACCCATCAAGCTCTACTGTAAAGGGGACGGCAGATGGCGTGGCCATCGGGGGCTAC     | 720  |
| Db | 728  | GTACCCATCAAGCTCTACTGTAAAGGGGACGGCAGATGGCGTGGCGATCGGGGGCTAC     | 787  |
| Qy | 721  | ATGAGCAAGCAGGCTCTGAGGCGCTTGAAGATGGACACGTCGTGCGCAGGTGTCCATCT    | 780  |
| Db | 788  | ATGTGCAGACAGGCTCTGAGGCGCTTGAAGATGGACACGTCGTGCGCAGGTGTCCATCT    | 847  |
| Qy | 781  | GGGACTTTCAGGGCCCAACCAAGGGGATGAGGCTGTACCACTGTCCCATCAACACCGG     | 840  |
| Db | 848  | GGGACTTTCAGGGCCCAACCAAGGGGATGAGGCTGTACCACTGTCCCATCAACACCGG     | 907  |
| Qy | 841  | ACCACTTCTAAGGGGCGACACAACTGTGTCTGCGCCATGTGCTACTACAGAGACACTG     | 900  |
| Db | 908  | ACCACTTCTAAGGGGCGCGACAACTGTGTCTGCGCCATGTGCTACTACAGAGACACTG     | 967  |
| Qy | 901  | GACCCCGTGAACATGCGCTGCACAAACCATCCCTCCGGCCCGACGGCTGTATTTCAGT     | 960  |
| Db | 968  | GACCCCGTGAACATGCGCTGCACAAACCATCCCTCCGGCCCGACGGCTGTATTTCAGT     | 1027 |
| Qy | 961  | GTCATAGAGACCTCCCTCATGCTGTGAGTGGACCCCTCCCCCGACTCCGGAGGCGGAG     | 1020 |
| Db | 1028 | GTCATAGAGACCTCCCTCATGCTGTGAGTGGACCCCTCCCCCGACTCCGGAGGCGGAG     | 1087 |
| Qy | 1021 | GACCTGCTTAAACATCACTGTGACAGACTGTGGCTGGGGCGGGGGGCTTGACACCGC      | 1080 |
| Db | 1088 | GACCTGCTTAAACATCACTGTGACAGACTGTGGCTGGGGCGGGGGGCTTGACACCGC      | 1147 |
| Qy | 1081 | TGCGGGGACATGTACAGTACGGACCGACCGCAATAGGCTGTACCGACCGACCATTTAC     | 1140 |
| Db | 1148 | TGCGGGGACATGTACAGTACGGACCGACCGCAATAGGCTGTACCGACCGACCATTTAC     | 1207 |
| Qy | 1141 | ATCACTGACCTGTGCGCCACACCCAGATACCTTGGATGCCAGATCCAGGCTGAAGGGGTT   | 1200 |
| Db | 1208 | ATCACTGACCTGTGCGCCACACCCAGATACCTTGGATGCCAGATCCAGGCTGTAAAGGGGTT | 1267 |
| Qy | 1201 | ACTGACGAGACCCCTTCTGCGCTCGAGTTGCGCTGTGTAAATCAACCAACCAACAGCA     | 1260 |
| Db | 1268 | ACTGACGAGACCCCTTCTGCGCTCGAGTTGCGCTGTGTAAATCAACCAACCAACAGCA     | 1327 |
| Qy | 1261 | GCTTCATGGGACATGTCCATCATGATCAGTGAAGCGCGACCGTGGAGACATTAACCTG     | 1320 |
| Db | 1328 | GCTTCATGGGACATGTCCATCATGATCAGTGAAGCGCGACCGTGGAGACATTAACCTG     | 1387 |
| Qy | 1321 | TGCTGGTCCAGACCGGAGACGCCAATGGCGGTATCCTGGACATTAAGCTGTGAGTACAT    | 1380 |
| Db | 1388 | TGCTGGTCCAGACCGGAGACGCCAATGGCGGTATCCTGGACATTAAGCTGTGAGTACAT    | 1447 |
| Qy | 1381 | GAGAAGGAGCTACAGATACCAAGCCACAGCATAAAAAGGCCCAACCAACGGTGTAC-      | 1439 |
| Db | 1448 | GAGAAGGAGCTACAGATACCAAGCCACAGCATAAAAAGGCCCAACCAACGGTGTAC-      | 1507 |
| Qy | 1440 | -----GGGCGTCAAAAGCCGGGCGCCATATGTCTTCCAGGTGGCGGACGCACTGTGGCA    | 1494 |
| Db | 1508 | GTGCAAGGCGCTCAAAAGCCGGGCGCCATATGTCTTCCAGGTGGCGGACGCACTGTGGCA   | 1567 |
| Qy | 1495 | GCGTACGGGCGCTACAGCGGCAATGTACTTCCAGACCATGACAGAAACGAGTACAG       | 1554 |
| Db | 1568 | GCGTACGGGCGCTACAGCGGCAATGTACTTCCAGACCATGACAGAAACGAGTACAG       | 1627 |
| Qy | 1555 | ACAAGATCCAGAGAAAGTGCACATCATGGGTCGCTCGGCGCTGGCTGTGCTTC          | 1614 |
| Db | 1628 | ACAAGATCCAGAGAAAGTGTGCACTCATCGGCTCTCGGCGCTGGCTGTGCTTC          | 1687 |
| Qy | 1615 | CTCATTTGCTGTGTGTTCATGGCCATGCTGTAAACAGACGGGGGTTTGAAGCTGTGAC     | 1674 |

Db 1688 CTCATTGCTGTGTGTCATGCGCATTGTTGTAACAGACGGGGTTTGAGCGTCTGAC 1747  
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 ACCESSION AX034853  
 VERSION AX034853.1 GI:11190805  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE Vinals, Y.D.  
 AUTHORS Novel uses  
 TITLE Patent: WO 0053216-A 1 14-SEP-2000;  
 JOURNAL SMITHKLINE BECHAM BIOLOG (BE) ; VINALS Y DE BASSOLS CARLOTA (BE)  
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 Qy 361 TGGGGAAGGTGATACATTCGACCGGAGAGAGCTTTCGCCAGGTGAGCTGGGCTGGC 420  
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 Db 567 CGGCTCATGAATAATCAACACCGAGGTGCGAGGCTTGGAGCTGTGCTCGCAGCGGCTTC 626



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|----|------|--|------|
| QY | 481  | TACCTGGCCCTCCAGGACTATGCGGGCTGACATGTCCCTCATCGCCGTCGTGCTTCTAC  | 540  |
| Db | 627  | TACCTGGCCCTCCAGGACTATGCGGGCTGACATGTCCCTCATCGCCGTCGTGCTTCTAC  | 686  |
| QY | 541  | CGCAAGTCCCCCGCATCTCATCCGAATAAGGCGCATCTTCAGGAAACCGTGTGGGGGCT  | 600  |
| Db | 687  | CGCAAGTCCCCCGCATCTCATCCGAATAAGGCGCATCTTCAGGAAACCGTGTGGGGGCT  | 746  |
| QY | 601  | GAGAGCAATCCGTGTGGCTCCCGGGGACAGTGCATCGCCCAATGCGGAAGATGGAT     | 650  |
| Db | 747  | GAGAGCAATCCGTGTGGCTCCCGGGGACAGTGCATCGCCCAATGCGGAAGATGGAT     | 806  |
| QY | 661  | GTACCCATCAAGCTTACTGTAAAGGGGACGGCAGTGGCTGTGCCATCGGGCGCTGC     | 720  |
| Db | 807  | GTACCCATCAAGCTTACTGTAAAGGGGACGGCAGTGGCTGTGCCATCGGGCGCTGC     | 866  |
| QY | 721  | ATGTGCAAGACAGCTTCGAGGCCGCTTGAGATGGACACGTCGTGCGAGGTGTGCATCT   | 780  |
| Db | 867  | ATGTGCAAGACAGCTTCGAGGCCGCTTGAGATGGACACGTCGTGCGAGGTGTGCATCT   | 926  |
| QY | 781  | GGGACTTTCAGGCGCAACCAAGGGGATGAGGCTTACCCACTGTGCCATCAACAGCGG    | 840  |
| Db | 927  | GGGACTTTCAGGCGCAACCAAGGGGATGAGGCTTACCCACTGTGCCATCAACAGCGG    | 986  |
| QY | 841  | ACCACTTCTGAAGGGGCGCACCACTGTGTCTCGCCCAATGGCTACTACAGAGCAGACTG  | 900  |
| Db | 987  | ACCACTTCTGAAGGGGCGCACCACTGTGTCTCGCCCAATGGCTACTACAGAGCAGACTG  | 1046 |
| QY | 901  | GACCCCTTGACATGGCCGTGCACAAACCATCCCTCGGGCGCCAGGCTGTATTTCAGT    | 960  |
| Db | 1047 | GACCCCTTGACATGGCCGTGCACAAACCATCCCTCGGGCGCCAGGCTGTATTTCAGT    | 1106 |
| QY | 961  | GTCAATGAGACCTCCCTCATGCTGAGTGGAGCCCTCCCGCGACATCCGAGCGCGAG     | 1020 |
| Db | 1107 | GTCAATGAGACCTCCCTCATGCTGAGTGGAGCCCTCCCGCGACATCCGAGCGCGAG     | 1166 |
| QY | 1021 | GACCTGCTTACAACATCATCTGCAAGAGCTGTGGCTGGGGCGGGGGTCTGTCAACCCG   | 1080 |
| Db | 1167 | GACCTGCTTACAACATCATCTGCAAGAGCTGTGGCTGGGGCGGGGGTCTGTCAACCCG   | 1226 |
| QY | 1081 | TGGGGGACAAATGTAAGTACGACGACACGCGCATAGGCGTCAACGACCAACGGATTAC   | 1140 |
| Db | 1227 | TGGGGGACAAATGTAAGTACGACGACACGCGCATAGGCGTCAACGACCAACGGATTAC   | 1286 |
| QY | 1141 | ATCAGTAGACCTGTGGGCCACACCCAGTACACCTTCGAGATCCAGGCTGTGAAGGCGTT  | 1200 |
| Db | 1287 | ATCAGTAGACCTGTGGGCCACACCCAGTACACCTTCGAGATCCAGGCTGTGAAGGCGTT  | 1346 |
| QY | 1201 | ACTGACAGAGCCCCCTTCTGCGCTCAAGTTCGCCCTCTGTGTAACATCAACCAACGAGCA | 1260 |
| Db | 1347 | ACTGACAGAGCCCCCTTCTGCGCTCAAGTTCGCCCTCTGTGTAACATCAACCAACGAGCA | 1406 |
| QY | 1261 | GCTCATTCGGCAGTGTCCATCATGATGTAAGGAGCGGACCGTAGAGCATTAACCTG     | 1320 |
| Db | 1407 | GCTCATTCGGCAGTGTCCATCATGATGTAAGGAGCGGACCGTAGAGCATTAACCTG     | 1466 |
| QY | 1321 | TCTGTGTCCAGCCGAGCAGGCCAATGGCGTGAATCTGGAATATGAGCTGCAGTACTAT   | 1380 |
| Db | 1467 | TCTGTGTCCAGCCGAGCAGGCCAATGGCGTGAATCTGGAATATGAGCTGCAGTACTAT   | 1526 |
| QY | 1381 | GAGAAGAGCTCAGTGTGTACAAGGCCACAGCCATTAAGAGCCCAACCAACGCTGAC-    | 1439 |
| Db | 1527 | GAGAAGAGCTCAGTGTGTACAAGGCCACAGCCATTAAGAGCCCAACCAACGCTGAC     | 1586 |
| QY | 1440 | -----GGGCTCAAGAGCCGGCGGCATCTAATGCTTCCAGAGTGGGGGACGACGTGGCA   | 1494 |
| Db | 1587 | GTGCAAGGCTCAAGAGCCGGCGGCATCTAATGCTTCCAGAGTGGGGGACGACGCTGGCA  | 1646 |
| QY | 1495 | GGCTACGGGCGCTACACGGCGAAGATGTACTTCAACCATGACAGAAAGCGGATGACAG   | 1554 |
| Db | 1647 | GGCTACGGGCGCTACACGGCGAAGATGTACTTCAACCATGACAGAAAGCGGATGACAG   | 1706 |

|    |      |   |      |
|----|------|---|------|
| QY | 1555 | ACAAGCATCCAGAGAAAGTTGGCCACTCATCATTCGGCTCTCTGGGGCGGTGGCTGGTCTTC    | 1614 |
| Db | 1707 | ACAAGCATCCAGAGAAAGTTGGCCACTCATCATTCGGCTCTCTGGGGCGGTGGCTGGTCTTC    | 1766 |
| QY | 1615 | CTCATTCCTGTGGTGGTGCATTCGGCATCGTGTATAC---AGACGGGGGTTTGAACGCTGT     | 1671 |
| Db | 1767 | CTCATTCCTGTGGTGGTGCATTCGGCATCGTGTATACCAAGACGGGGGTTTGAACGCTGT      | 1826 |
| QY | 1672 | GACTCGGAGTACACGGAGCAAGCTGCACACACTACACAGTGGCCCATTAACCCAGCGATG      | 1731 |
| Db | 1827 | GACTCGGAGTACACGGAGCAAGCTGCACACACTACACAGTGGCCCATTAACCCAGCGATG      | 1886 |
| QY | 1732 | AAGATCTACATCGATTCCTTTACCTTACGAGAGACCCCAACGAGCGCATGTGGGATTTGCC     | 1791 |
| Db | 1887 | AAGATCTACATCGATTCCTTTACCTTACGAGAGACCCCAACGAGCGCATGTGGGATTTGCC     | 1946 |
| QY | 1792 | AAGAAATTGACATCTCCCTGTGCANAAATTGAGACAGGTGATCGGACAGGGGATTTGGC       | 1851 |
| Db | 1947 | AAGAAATTGACATCTCCCTGTGCANAAATTGAGACAGGTGATCGGACAGGGGATTTGGC       | 2006 |
| QY | 1852 | GAGGCTGCAGTGGCCACCTGAAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAG        | 1911 |
| Db | 2007 | GAGGCTGCAGTGGCCACCTGAAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAG        | 2066 |
| QY | 1912 | ACGCTCAAGTCCGGGCTACACGGAGAAAGCAGCGCCGGACTTCTGTAGGAGACCTTCATC      | 1971 |
| Db | 2067 | ACGCTCAAGTCCGGGCTACACGGAGAAAGCAGCGCCGGACTTCTGTAGGAGACCTTCATC      | 2126 |
| QY | 1972 | ATGGGCGAGTTCGCACATCTCCACAGTCAATCCACTTGSAGAGGTGTGTACCAAGACACA      | 2031 |
| Db | 2127 | ATGGGCGAGTTCGCACATCTCCACAGTCAATCCACTTGSAGAGGTGTGTGTACCAAGACACA    | 2186 |
| QY | 2032 | CCTGTGATGATCATCACCGAGTTTCATGAGAAATGGCTCCCTGGACTCTTTCTCCGGCAA      | 2091 |
| Db | 2187 | CCTGTGATGATCATCACCGAGTTTCATGAGAAATGGCTCCCTGGACTCTTTCTCCGGCAA      | 2246 |
| QY | 2092 | AACGATGGGCGATTACAGATCATTCAGAGCTGTGTGGGATGCTTCCGGGGCATGGCAGCTGGC   | 2151 |
| Db | 2247 | AACGATGGGCGATTACAGAGTCAATTCAGAGCTGTGTGGGATGCTTCCGGGGCATGGCAGCTGGC | 2306 |
| QY | 2152 | ATGAAGTACCGGGGACATGAACTATGTTTCAACCGTGACTGGCTGGCCGCAACATCTCTC      | 2211 |
| Db | 2307 | ATGAAGTACCGGGGACATGAACTATGTTTCAACCGTGACTGGCTGGCCGCAACATCTCTC      | 2366 |
| QY | 2212 | GTCACACAGCAACTGTGTCGACAGAGTGTGCGACTTTGGGCTCTCAAGCTTTCTAGAGAGAC    | 2271 |
| Db | 2367 | GTCACACAGCAACTGTGTCGACAGAGTGTGCGACTTTGGGCTCTCAAGCTTTCTAGAGAGAC    | 2426 |
| QY | 2272 | GATACCTTCAGACCCCACTTACACCAAGTGGCCCTGTGGCGGAAAGTTCCCATCCGCTGACACA  | 2331 |
| Db | 2427 | GATACCTTCAGACCCCACTTACACCAAGTGGCCCTGTGGCGGAAAGTTCCCATCCGCTGACACA  | 2486 |
| QY | 2332 | GGCCCGGAAGCATTCACAGTCCGGAAGTTCACTCGGGCCAGATGTGTGGAGGACGACG        | 2391 |
| Db | 2487 | GGCCCGGAAGCATTCACAGTCCGGAAGTTCACTCGGGCCAGATGTGTGTGGAGGCTACGGC     | 2546 |
| QY | 2392 | ATTGTCAATGAGAGATGTCTCTATAGGGAGACGGCCCTACTGTGGACATGACCAACACG       | 2451 |
| Db | 2547 | ATTGTCAATGAGAGATGTCTCTATAGGGAGACGGCCCTACTGTGGACATGACCAACACG       | 2606 |
| QY | 2452 | GATGTAAATCAATGCCATTTAGACAGAGACTATCGGCTGCCACCGCCCATGTGATCGCCGACG   | 2511 |
| Db | 2607 | GATGTAAATCAATGCCATTTAGACAGAGACTATCGGCTGCCACCGCCCATGTGATCGCCGACG   | 2666 |
| QY | 2512 | GGCCGTCACCAATCATGTGAGGATGTGTGGCACAAGAGCGGAACACACCGGGCCCAAGTTTC    | 2571 |
| Db | 2667 | GGCCGTCACCAATCATGTGAGGATGTGTGGCACAAGAGCGGAACACACCGGGCCCAAGTTTC    | 2726 |
| QY | 2572 | GGCCAAATTTGTCAACACGCTTACAGCAAGATATCCGAAATCCCAACAGCTCTCAAAAGCCATG  | 2631 |
| Db | 2727 | GGCCAAATTTGTCAACACGCTTACAGCAAGATATCCGAAATCCCAACAGCTCTCAAAAGCCATG  | 2786 |
| QY | 2632 | GGCGCCCTCTCTCTGGCATTCACCTTGCCTGGCTCTGTGACCGCACATCTCCCGCATTCACCC   | 2691 |



|||||  
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Db 2907 TTCCCAATGCGGCTTCCCTTGTGACGTCTGTCTGATGATGATGAGAGACATT 2966  
OY 2812 CTCGGGGTGGGGTCACTTTGGCTGGCCACCAGAAAAAATCTGAACAGTATCAGGTG 2871  
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DEFINITION Homo sapiens (clone FBK III 11c) protein-tyrosine kinase (DRT)  
ACCESSION L41939  
VERSION L41939.1 GI:1100109  
KEYWORDS DRT gene; EPH gene family; protein-tyrosine kinase.  
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REFERENCE 1 (bases 1 to 3768)  
AUTHORS Ikegaki,N., Tang,X.X., Iltis,J.A., Allen,C., Yoshida,A., Sulman,E.P., Brodeur,G.M. and Pleasure,D.E.  
TITLE Molecular characterization and chromosomal localization of DRT (EPH3): a developmentally regulated human protein-tyrosine kinase gene of the EPH family  
JOURNAL Hum. Mol. Genet. 4 (11), 2033-2045 (1995)  
MEDLINE 96154673  
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Matches 2956; Conservative 0; Mismatches 6; Indels 9; Gaps 2;  
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Db 147 CTGCTGCGCCCGCTGGAAGAAAGCTAATGAGATCCACTACAGCGACTGTGAGCTGGGC 206  
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|    |      |   |      |
|----|------|---|------|
| QY | 721  | ATGTGCMAAGCAGCGCTTGCAGGCCCTTTAGAAATGGCACACCTGTCTGCCAGATTTTCCATCT  | 780  |
| Db | 867  | ATTGTGCMAAGCAGCGCTTGCAGGCCCTTTAGAAATGGCACACCGTCTGCCAGATTTTCCATCT  | 926  |
| QY | 781  | GGGACCTTTCAAGGCCCAACCAAGGGATGAGGCTGTACCCACTGTCTCCATCAACACCGG      | 840  |
| Db | 927  | GGGACCTTTCAAGGCCCAACCAAGGGATGAGGCTGTACCCACTGTCTCCATCAACACCGG      | 986  |
| QY | 841  | ACCACTTCTGAAGGGGCCACCAACTGTGTCTGCCCAATGGCTACTACAGAGACACTTG        | 900  |
| Db | 987  | ACCACTTCTGAAGGGGCCACCAACTGTGTCTGCCCAATGGCTACTACAGAGACACTTG        | 1046 |
| QY | 901  | GACCCCCGTGACATGCGCTCTGCACAAACATCTCCCTCTCGGGCCCCAGGCTGTGATTTCCAGT  | 960  |
| Db | 1047 | GACCCCCGTGACATGCGCTCTGCACAAACATCTCCCTCTCGGGCCCCAGGCTGTGATTTCCAGT  | 1106 |
| QY | 961  | GTCMAATGAGACCTCCCTCATGTGTGGAGTGGACCCCTCCCGCGACTCCGGAGGCGCGAG      | 1020 |
| Db | 1107 | GTCMAATGAGACCTCCCTCATGTGTGGAGTGGACCCCTCCCGCGACTCCGGAGGCGCGAG      | 1166 |
| QY | 1021 | GACCTGTCTACAMACTATCTTGCAGAGCTGTGGCTTGGGCCGGGGTGTCTGCACCCG         | 1080 |
| Db | 1167 | GACCTGTCTACAMACTATCTTGCAGAGCTGTGGCTTGGGCCGGGGTGTCTGCACCCG         | 1226 |
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| QY | 1141 | ATCAGTGAACCTGTGTGGCCCAACCCAGTACACCTTCGAGATCTCAAGGCTGTGAACGGGCTT   | 1200 |
| Db | 1287 | ATCAGTGAACCTGTGTGGCCCAACCCAGTACACCTTCGAGATCTCAAGGCTGTGAACGGGCTT   | 1346 |
| QY | 1201 | ACTGACGAGAGCCCTTCTTCTGCGCTCAGTTGCGCTCTGTGAACATCTACCACCAACAGACA    | 1260 |
| Db | 1347 | ACTGACGAGAGCCCTTCTTCTGCGCTCAGTTGCGCTCTGTGAACATCTACCACCAACAGACA    | 1406 |
| QY | 1261 | GCTTCATCGGCACTGTTCATCATGCACTCAGGTGAGCCGCAACCGTGGAGCAGCATTTACCTTG  | 1320 |
| Db | 1407 | GCTTCATCGGCACTGTTCATCATGCACTCAGGTGAGCCGCAACCGTGGAGCAGCATTTACCTTG  | 1466 |
| QY | 1321 | TCTGTGTGCCAGCGGACCAAGCCCAATGGCGGTGATCTCGAGACTATGAGCTGCATTAAT      | 1380 |
| Db | 1467 | TCTGTGTGCCAGCGGACCAAGCCCAATGGCGGTGATCTCGAGACTATGAGCTGCATTAAT      | 1526 |
| QY | 1381 | GAGAAAGAGCTCAGTAGTACAAAGCCACAGCCATTAATAAGCCGCCACCAACACGCTCAC-     | 1439 |
| Db | 1527 | GAGAAAGAGCTCAGTAGTACAAAGCCACAGCCATTAATAAGCCGCCACCAACACGCTCAC      | 1586 |
| QY | 1440 | -----GGGCTCTCAAGCGCGGCGCATCTATGTCTTTCAGAGTGGGGCACGCACTGTGGCA      | 1494 |
| Db | 1587 | GTGCAAGGGCTCTCAAGCGCGGCGCATCTATGTCTTTCAGAGTGGGGCACGCACTGTGGCA     | 1646 |
| QY | 1495 | GGCTACGGGGGCTACAGCGGCAAGATGTACTTCAGACCATGACAGAAAGCGGAGTACCAG      | 1554 |
| Db | 1647 | GGCTACGGGGGCTACAGCGGCAAGATGTACTTCAGACCATGACAGAAAGCGGAGTACCAG      | 1706 |
| QY | 1555 | ACAAGCATCCAGAGAGAGTTGGCACTACATCTGGCTCTCGGCGCTGAGGCTGTCTTC         | 1614 |
| Db | 1707 | ACAAGCATCCAGAGAGAGTTGGCACTACATCTGGCTCTCGGCGCTGAGGCTGTCTTC         | 1766 |
| QY | 1615 | CTCATGTGCTGTGGTTGTTCATCGCCATCGTGTGTAACT--AGACGGGGGTTTGAACGCTGT    | 1671 |
| Db | 1767 | CTCATGTGCTGTGGTTGTTCATCGCCATCTGTGTGTAACTAGAAAGACGGGGGTTTGAACGCTGT | 1826 |
| QY | 1672 | GACTCGGAGTACAGGAGCAAGTGCAGAACTACACAGTGGGCAACATTAACCCAGGAGATG      | 1731 |
| Db | 1827 | GACTCGGAGTACAGGAGCAAGTGCAGAACTACACAGTGGGCAACATTAACCCAGGAGATG      | 1886 |
| QY | 1732 | AAGATCTACATCGATCTCTTTCACCTACGAGAGACCCCAAGAGGCACTGGGAGATTGTGC      | 1791 |
| Db | 1887 | AAGATCTACATCGATCTCTTTCACCTACGAGAGACCCCAAGAGGCACTGGGAGATTGTGC      | 1946 |

|    |      |  |      |
|----|------|--|------|
| OY | 1792 | AAGAAATTGACATCTCTCTGTGTCAAAATTGACAGAGTGATCCGAGAGAGGGAGTTGGC    | 1891 |
| Db | 1947 | AAGGAAATTGACATCTCTCTGTGTCAAAATTGACAGAGTGATCCGAGAGGGAGTTGGC     | 2006 |
| OY | 1852 | GAGGCTCAGTGGCGACACTGAACCTGGCAGAGCAAGAGAGATCTTTGTGGCCATCAAG     | 1911 |
| Db | 2007 | GAGGCTCAGTGGCGACACTGAACCTGGCAGAGCAAGAGAGATCTTTGTGGCCATCAAG     | 2066 |
| OY | 1912 | ACGCTCAAGTGGGGCTACACGGAGAACGACGCGGGGACTTCGTAGCCGAAGCTCCATC     | 1971 |
| Db | 2067 | ACGCTCAAGTGGGGCTACACGGAGAACGACGCGGGGACTTCGTAGCCGAAGCTCCATC     | 2126 |
| OY | 1972 | ATGGGCGAGTTCGACACATCCCAAGCTCATCCACTGGAGGGGTGTGTGACCAAGAGACA    | 2031 |
| Db | 2127 | ATGGGCGAGTTCGACACATCCCAAGCTCATCCACTGGAGGGGTGTGTGACCAAGAGACA    | 2186 |
| OY | 2032 | CCTGTGATGATCATCACCAGAGTTCTATGGAGAATGGCTCCCTGAGACTCTTCTCGCGCA   | 2091 |
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| OY | 2092 | AACGATGGGCGAGTTTCACAGTCATCCAGCTGGTGGGCATGCTTCGGGGCATGCGAGCTGGC | 2151 |
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| OY | 2152 | ATGAAGTACCTTGGCGACATGAATATTTTACACGTGACTGTGCTGGCCCGCAACATCTTC   | 2211 |
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| OY | 2272 | GATACCTGAGACCCACCTACACACAGTCCCTGGGCGGAAAGTTTCCCATCCGCTGGACA    | 2331 |
| Db | 2427 | GATACCTGAGACCCACCTACACACAGTCCCTGGGCGGAAAGATCCCATCCGCTGGACA     | 2486 |
| OY | 2332 | GGCCCGGAAGCCATCCAGTACCCGGAAGTTTCACTTCGGCCAGTGATGTGTGGAGCTACGGC | 2391 |
| Db | 2487 | GGCCCGGAAGCCATCCAGTACCCGGAAGTTTCACTTCGGCCAGTGATGTGTGGAGCTACGGC | 2546 |
| OY | 2392 | ATTGTGATGTGGAGGTATGTGTCATATGGGGGCGGGCCCTACTGGGACATGACCAACAG    | 2451 |
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| OY | 2452 | GATGTAAATCAATGACCATTTGAGCAGGACTATCGGCTGCCACCGCCCATGGACTGCCGAGC | 2511 |
| Db | 2607 | GATGTAAATCAATGACCATTTGAGCAGGACTATCGGCTGCCACCGCCCATGGACTGCCGAGC | 2666 |
| OY | 2512 | GGCCTGCACCAACTGATGCTGTGATGTTGGCAGAAAGACCGCACACCGGCCCAAGTTTC    | 2571 |
| Db | 2667 | GGCCTGCACCAACTGATGCTGTGATGTTGGCAGAAAGACCGCACACCGGCCCAAGTTTC    | 2726 |
| OY | 2572 | GGGCAAAATGTCAACACGCTAGCAAAAGATGATCCGCAATCCCAACAGGCTCAAAACCATG  | 2631 |
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| OY | 2632 | GGGCCCCCTCTCCTTGGGCATCAACCTGCGCTGTGTGACCGCAGCATCCCGACTACAC     | 2691 |
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| Db | 2847 | AGCTTTAACACGGTGGACGATGGCTGTGAGGCGCATCAAGATGGGGCAGTACAAAGAGAC   | 2906 |
| OY | 2752 | TTTGCCAAATGGCGGGTTCACCTTCCTTTGACGTGTGTCTCAATGATGATGAGAGACATT   | 2811 |
| Db | 2907 | TTTGCCAAATGGCGGGTTCACCTTCCTTTGACGTGTGTCTCAATGATGATGAGAGACATT   | 2966 |
| OY | 2812 | CTTCGGGTTGGGGTCACTTTTGGCTGGCCACAGAAAAAAATCTGTACAGATATCCAGGTG   | 2871 |
| Db | 2967 | CTTCGGGTTGGGGTCACTTTTGGCTGGCCACAGAAAAAAATCTGTACAGATATCCAGGTG   | 3026 |
| OY | 2872 | ATGCGGGCGAGATGACCAAGATTCAGTCTGTGTGAGGTTTGAATTTACCTGCTCGGCT     | 2931 |

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RESULT 8
LOCUS HUMERKA 3151 bp mRNA PRI 01-FEB-2000
DEFINITION Human mRNA for tyrosine kinase, complete cds.
ACCESSION D31661
VERSION D31661.1 GI:495677
KEYWORDS tyrosine kinase.
SOURCE Homo sapiens gastric cancer cell-line MKN28 CDNA to mRNA, clones
lambda ERK 5,6,7,HI.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Iwase,T., Tanaka,M., Suzuki,M., Naito,Y., Sugimura,H. and Kino,I.
TITLE Identification of protein-tyrosine kinase genes preferentially
JOURNAL expressed in embryo stomach and gastric cancer
MEDLINE Biochem. Biophys. Res. Commun. 194 (2), 698-705 (1993)
REFERENCE 2 (bases 1 to 3151)
AUTHORS Kiyokawa,E., Takai,S., Tanaka,M., Iwase,T., Suzuki,M., Xiang,Y.Y.,
Naito,Y., Yamada,K., Sugimura,H. and Kino,I.
TITLE Overexpression of ERK, an EPH family receptor protein tyrosine
JOURNAL kinase, in various human tumors
MEDLINE Cancer Res. 54 (14), 3645-3650 (1994)
REFERENCE 3 (bases 1 to 3151)
AUTHORS Kiyokawa,E.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Etsuko
MEDLINE Kiyokawa, Hamamatsu University School of Medicine, First Department
REFERENCE of Pathology; 3600 Handa cho, Hamamatsu, Shizuoka 431-31, Japan
AUTHORS (Tel:81-53-435-2220, Fax:81-53-435-2225)
JOURNAL Submitted (28-May-1994) to DDBJ by:
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First Department of Pathology
3600 Handa-cho
Hamamatsu, Shizuoka 431-31
Japan
Phone: 053-435-2220
Fax: 053-435-2225.

FEATURES
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OY 78 ATCAGGCTGGGAGAGAGTGTGAGTACGATGAGAACATGACATCCGACGATACCA
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|    |      |   |      |
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| Db | 786  | CGAGGCGCTTGAGAAATGAGACCGTCTGCCGAGGTTGTCCATCTGGGACTTTCAAGGCGCA     | 845  |
| QY | 798  | CCAAGGGGATGAGAGCCGTGTAACCACTGTCCATCAACAGCCGGACCACTTCTGAAGGGG      | 857  |
| Db | 846  | CCAAGGGGATGAGAGCCGTGTAACCACTGTCCATCAACAGCCGGACCACTTCTGAAGGGG      | 905  |
| QY | 858  | CACCAACTGTGTCTGCCGCAATGGCTACTACAGAGCAGACCTGGACCCCTTGGACATGGC      | 917  |
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| QY | 918  | CTGACACAACCATCCCTCCGGCGGCCCAAGGCTGTGAATTCAGATGCATATGAGACCTCCCT    | 977  |
| Db | 966  | CTGACACAACCATCCCTCCGGCGGCCCAAGGCTGTGAATTCAGATGCATATGAGACCTCCCT    | 1025 |
| QY | 978  | CATGCTTGAGTGGACCCCTCCCGCGCATCTCCGAGGCGCGAGAGGACCTCGTCAACAT        | 1037 |
| Db | 1026 | CATGCTTGAGTGGACCCCTCCCGCGCATCTCCGAGGCGCGAGAGGACCTCGTCAACAT        | 1085 |
| QY | 1038 | CATCTGCAGAGCTGTGTGCTTCGGGGCCGGGGGTGCTTGACACCGCTTCGGGGACATGTACA    | 1097 |
| Db | 1086 | CATCTGCAGAGCTGTGTGCTTCGGGGCCGGGGGTGCTTGACACCGCTTCGGGGACATGTACA    | 1145 |
| QY | 1098 | GTAGGCAACACGCGCAGCTAGGCTCTGACCCAGCAGCAGCATTTACATCACTGACCTGTGCGC   | 1157 |
| Db | 1146 | GTAGGCAACACGCGCAGCTAGGCTCTGACCCAGCAGCAGCATTTACATCACTGACCTGTGCGC   | 1205 |
| QY | 1158 | CCACACCCAGTACACCTTTGGAGATCCAAGCTGTGAACGGCGTTACTGACACAGAGCCCTT     | 1217 |
| Db | 1206 | CCACACCCAGTACACCTTTGGAGATCCAAGCTGTGAACGGCGTTACTGACACAGAGCCCTT     | 1265 |
| QY | 1218 | CTGCGCTCAGTTGCGCCCTCTGTGAACATCAACACCAACAGGAGGCTCATGCGGAGTGTG      | 1277 |
| Db | 1266 | CTGCGCTCAGTTGCGCCCTCTGTGAACATCAACACCAACAGGAGGCTCATGCGGAGTGTG      | 1325 |
| QY | 1278 | CATCATGCATCAGGTGAGCCGCGACCCGTGGACAGCATTAACCTGTGCTGTGCCAGCCGGA     | 1337 |
| Db | 1326 | CATCATGCATCAGGTGAGCCGCGACCCGTGGACAGCATTAACCTGTGCTGTGCCAGCCGGA     | 1385 |
| QY | 1338 | CCAGGCCAAATGGCGCTGATTCCTGGACATATGAGCTGCAGTACTATTTGAGA---AGSAGCTAG | 1394 |
| Db | 1386 | CCAGGCCAAATGGCGCTGATTCCTGGACATATGAGCTGCAGTACTATTTGAGA---AGSAGCTAG | 1445 |
| QY | 1395 | TGAGTACAAACGCCACAGCCATATAAAAGCCCCACCAACAGCGTAC-----GGGCTTCAA      | 1448 |
| Db | 1446 | TGAGTACAAACGCCACAGCCATATAAAAGCCCCACCAACAGCGTAC-----GGGCTTCAA      | 1505 |
| QY | 1449 | AGCGGGCCCATCTATGTCTTCCAGAGTGTGGGGGACCCACTGTGGCAGGTAACGGGGCGTA     | 1508 |
| Db | 1506 | AGCGGGCCCATCTATGTCTTCCAGAGTGTGGGGGACCCACTGTGGCAGGTAACGGGGCGTA     | 1555 |
| QY | 1509 | CAGCGGCAAGATGTACTTCCAGACATGACAGAGAAGCGGAGTACACAGACAAAGCATCAGGA    | 1568 |
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| QY | 1569 | GAAGTTGCCACTCATCATCGGCTCTCGCGCGCTGCGCTGTGCTTCCTCATATGCTGTGCT      | 1628 |
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| Db | 1746 | CAAGCTGCACACTACACCAAGTGGCCACATTAACCCAGGCAATGAGATCTACATCATTC       | 1805 |
| QY | 1749 | TTTTCACCTACAGAGAGCCCAACAGAGGAGTGGGGAGTTTGGCAAGGAATTTGACATTC       | 1808 |
| Db | 1806 | TTTTCACCTACAGAGAGCCCAACAGAGGAGTGGGGAGTTTGGCAAGGAATTTGACATTC       | 1865 |
| QY | 1809 | CTGTCTCAAAATTGAGCAGGTGATCGGAGCAGGGGAGTTTGGCAGGCTCGCAGTGGCA        | 1868 |

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| Db | 1866 | CTGTGTCMAAATTGACACGAGTATCGAGACAGGGGAGTTTGGGAGGTCGTGACGTGGCCA     | 1925 |
| Qy | 1869 | CTGTGAACCTGCCAGGCAAGAGAGATCTTTTGTGGCCATCAAGACGTCAAATGTGGGCTA     | 1928 |
| Db | 1926 | CTGTGAAGCTGCCAGGCAAGAGAGATCTTTTGTGGCCATCAAGACGTCAAATGTGGGCTA     | 1985 |
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| Db | 1986 | CACGGAAACACACGGCCGGGACTCTCTGAGCGAAGCCCTTCATCATATGGGCGCAATTCGACCA | 2045 |
| Qy | 1989 | TCCCAACGTCATCCACTGGAGGGTGTCTGTACCAAGAGCACACCTGTGATGATCATCAC      | 2048 |
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| Qy | 2109 | AGTCATCCAGCTGTGGGCGATGCTTGGGGGCATATCCAGCTGGCATATGAATACCTGGCAGA   | 2168 |
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| Db | 2286 | CTGCAAGGTGTGGAGCTTTTGGGCTCTCAGCGCTTTCTTAAGAGACATACCTGACAGCCAC    | 2345 |
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| Qy | 2349 | GTACCGGAAGTTTCAACCTCGGCGCATGATGTGAGGAGCTAACGCGATTTTCATGTGGAGGT   | 2408 |
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| Db | 2526 | TGAGCAGAGCATATCGGCTGGCACCGCCCAATGGATGCCGACCGCCCTGACCAACATCAT     | 2585 |
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| Qy | 2829 | TTTGGCTGGCCACCAAGAAAAATCTCTGAACAGTATCAAGTGTATGCGGGCGCAGATGAA     | 2888 |
| Db | 2886 | TTTGGCTGGCCACCAAGAAAAATCTCTGAACAGTATCAAGTGTATGCGGGCGCAGATGAA     | 2945 |
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DEFINITION Homo sapiens mRNA for large erk/ceks tyrosine kinase, partial cds.  
ACCESSION D37827  
VERSION D37827.1 GI:1060894  
KEYWORDS large erk/ceks tyrosine kinase.  
SOURCE Homo sapiens 4-month fetal brain cDNA to mRNA, clone\_11b:lambda  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Saito,T.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-1994) to the DDBJ/EMBL/GenBank databases.  
AUTHORS Toshiyuki Saito, National Institute of Radiological Sciences; 9-1  
Anagawa 4-chome, Inage-ku, Chiba 263, Japan  
(Tel:043-251-2111(ex.361), Fax:043-256-8301)  
2 (sites)  
Chap,J. and Watt,V.M.  
erk and erk. new members of the eph subclass of receptor  
protein-tyrosine kinases  
Oncogene 6 (6), 1057-1061 (1991)  
JOURNAL MEDLINE  
91296384  
AUTHORS Iwase,T., Tanaka,M., Suzuki,M., Naito,Y., Sugimura,H. and Kino,I.  
TITLE Identification of protein-tyrosine kinase genes preferentially  
expressed in embryo stomach and gastric cancer  
Biochem. Biophys. Res. Commun. 194 (2), 698-705 (1993)  
JOURNAL MEDLINE  
93343925  
AUTHORS Saito,T., Naohiko,S., Kitahara,M., Murata,M., Yamamoto,Y., Hori,T.  
and Matsuda,Y.  
TITLE Identification of human erk gene as a putative receptor tyrosine  
kinase and its chromosomal localization to 1p36.1: a comparative  
mapping of human, mouse and rat chromosomes  
Unpublished (1994)  
JOURNAL On Nov 13, 1995 this sequence version replaced gi:529066.  
COMMENT Submitted (01-AUG-1994) to DDBJ by:  
Toshiyuki Saito  
National Institute of Radiological Sciences  
Division of Genetics  
9-1 Anagawa 4-chome, Inage-ku  
Chiba 263  
Japan  
Phone: 043-251-2111 x333  
Fax: 043-251-9818.  
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Db 13 GTGCGAGGCTACGAGGCGCTACGCGGCAAGATGTACTTCAGACCATGACAGAGCGAG 72  
OY 1549 TACCAAGCAAGCATCCAGAGAGAGTTGCCATCATCGCTCTCGGCGCTGCGCTG 1608  
Db 73 TACCAGACAAGCATCCAGAGAGAGTTGCCATCATCGCTCTCGGCGCTGCGCTG 132  
OY 1609 GTCTTCCTATGCTGT 1668  
Db 133 GTCTTCCTATGCTGT 192  
OY 1669 GCTGACTCGAGTACACGAGACGAGACGAGTGCACACTACACGAGTGCACACTACAC 1728  
Db 193 GCTGACTCGAGTACACGAGACGAGACGAGTGCACACTACACGAGTGCACACTACAC 252  
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Db 253 ATGAAATCTACATGATCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 312  
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Db 313 GCCAAGAAATGACATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 372  
OY 1849 GGGAGAGTGTGAGTGGCCACCTGAGAGTGCAGAGGCAAGAGAGATCTTTGTGGCATC 1908  
Db 373 GGGAGAGTGTGAGTGGCCACCTGAGAGTGCAGAGGCAAGAGAGATCTTTGTGGCATC 432  
OY 1909 AAGAGCCTTAAGTGTGGGCTTACACGAGAGAGAGCGCGGAGATCTTCTGTAGCAAGCTTC 1968  
Db 433 AAGAGCCTTAAGTGTGGGCTTACACGAGAGAGAGCGCGGAGATCTTCTGTAGCAAGCTTC 492  
OY 1969 ATCATGAGGCGAGTGTGACCATCCCAAGCGTATCCACTGAGAGGAGTGTGTGTGTGTGT 2028  
Db 493 ATCATGAGGCGAGTGTGACCATCCCAAGCGTATCCACTGAGAGGAGTGTGTGTGTGTGT 552  
OY 2029 ACACCTGTGATGATCATCACGAGTTCATGAGAAATGGCTCCCTGAGACTCTTTCTCCGG 2088  
Db 553 ACACCTGTGATGATCATCACGAGTTCATGAGAAATGGCTCCCTGAGACTCTTTCTCCGG 612  
OY 2089 CAAGAAGATGGGCACTTACATCATCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2148  
Db 613 CAAGAAGATGGGCACTTACATCATCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 672

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| OY | 2149 | GGCATGAAGTACCTGGGAGACATGATGTCACCGCTGGCTGCGCCGACATC          | 2208 |
| Db | 673  | GGCATGAAGTACCTGGGAGACATGATGTCACCGCTGGCTGCGCCGACATC          | 732  |
| OY | 2209 | CTCGTCAACACCACTGGTGTGCAAGGTGTGCACTTTGGGCTCTCACGCTTTCTAGAG   | 2268 |
| Db | 733  | CTCGTCAACACCACTGGTGTGCAAGGTGTGCACTTTGGGCTCTCACGCTTTCTAGAG   | 792  |
| OY | 2269 | GACGATACCTAGACCCCACTACACCAAGTCCCTGGGCGGAAAGTTCCCATCCGCTGG   | 2328 |
| Db | 793  | GACGATACCTAGACCCCACTACACCAAGTCCCTGGGCGGAAAGTTCCCATCCGCTGG   | 852  |
| OY | 2329 | ACAGCCCGGAAAGCCATCCAGTACCGGAAGTTCACCTCGCCAGTATGTGTGAGCTAC   | 2388 |
| Db | 853  | ACAGCCCGGAAAGCCATCCAGTACCGGAAGTTCACCTCGCCAGTATGTGTGAGCTAC   | 912  |
| OY | 2389 | GGCATTGTATGTGGAGGTGATGTCATATGGGAGCGGCGCTACTGGGACATGACCAAC   | 2448 |
| Db | 913  | GGCATTGTATGTGGAGGTGATGTCATATGGGAGCGGCGCTACTGGGACATGACCAAC   | 972  |
| OY | 2449 | CAGGATGTATATGATCCATTTGAGAGAGATGATGCGCTGGCCACCATGAGACTGCCG   | 2508 |
| Db | 973  | CAGGATGTATATGATCCATTTGAGAGAGATGATGCGCTGGCCACCATGAGACTGCCG   | 1032 |
| OY | 2509 | ACGCGCCCTGACCACTCATCTGCTGAGTGTGGCAGAAAGACCGCACCCGCGCCAAG    | 2568 |
| Db | 1033 | ACGCGCCCTGACCACTCATCTGCTGAGTGTGGCAGAAAGACCGCACCCGCGCCAAG    | 1092 |
| OY | 2569 | TTGCGGCCAAATTTGTCAACACGCTAGACAGATGATCCGCAATCCCAACAGCTCAAGCC | 2628 |
| Db | 1093 | TTGCGGCCAAATTTGTCAACACGCTAGACAGATGATCCGCAATCCCAACAGCTCAAGCC | 1152 |
| OY | 2629 | ATGGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  | 2688 |
| Db | 1153 | ATGGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  | 1212 |
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| Db | 1213 | ACCAGCTTTAACACGCTGAGCAGTGTGAGAGGCCATCAAGATGGGCGAGTACAAAGAG  | 1272 |
| OY | 2749 | AGCTTGCCCAATGCGGCTTACCTCTTGGAGTGTGTCTCAGATGATGATGAGAGAG     | 2808 |
| Db | 1273 | AGCTTGCCCAATGCGGCTTACCTCTTGGAGTGTGTCTCAGATGATGATGAGAGAG     | 1332 |
| OY | 2809 | ATTCTCGGGTGGGGTGCATTTGGCTGGCGACACAGAAAAAATCTGAACAGTATCCAG   | 2868 |
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| OY | 2869 | GTGATGCGGGCGAGATGAACAGATTCAGTGTGTGAGGTTTGACATTACCTGCTCG     | 2928 |
| Db | 1393 | GTGATGCGGGCGAGATGAACAGATTCAGTGTGTGAGGTTTGACATTACCTGCTCG     | 1452 |
| OY | 2929 | GCTCACTCTTCTCCCAAGCGCGCGCGCTCTCG                            | 2962 |
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LOCUS HUMERK 1225 bp mRNA PRI 23-JUN-1999  
DEFINITION Human mRNA for large erk kinase.  
ACCESSION D14717  
VERSION D14717.1 GI:285916  
KEYWORDS large erk kinase.  
SOURCE Homo sapiens gastric carcinoma, cDNA to mRNA, clone H1.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Chan, J. and Watt, V.M.  
TITLE erk and erk, new members of the eph subclass of receptor  
protein-tyrosine kinases  
JOURNAL Oncogene 6 (6), 1057-1061 (1991)

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|---------------------------|--|------|
| MEDLINE                   | 91296384   |      |
| REFERENCE                 | 2 (sites)  |      |
| AUTHORS                   | Iwase,T., Tanaka,M., Suzuki,M., Naito,Y., Sugimura,H. and Kino,I.  |      |
| TITLE                     | Identification of protein-tyrosine kinase genes preferentially expressed in embryo stomach and gastric cancer  |      |
| JOURNAL                   | Biochem. Biophys. Res. Commun. 194 (2), 698-705 (1993)   |      |
| MEDLINE                   | 93343925   |      |
| REFERENCE                 | 3 (bases 1 to 1225)  |      |
| AUTHORS                   | Iwase,T.   |      |
| JOURNAL                   | Unpublished (1993)   |      |
| COMMENT                   | Submitted (23-MAR-1993) to DDBJ by:<br>Toshio Iwase<br>First Department of Pathology<br>Hamamatsu University<br>School of Medicine<br>3600 Handa-cho, Hamamatsu<br>Shizuoka 431-31<br>Japan<br>Phone: 053-435-2220<br>Email: toiwase@ddbj.nig.ac.jp<br>Fax: 053-435-2225.<br>Location/Qualifiers<br>1..1225<br>/organism="Homo sapiens"<br>/db_xref="taxon:9606"<br>/tissue_type="gastric carcinoma"<br>1..1044<br>/gene="large erk"<br><1..1044<br>/gene="large erk"<br>/function="protein-tyrosine kinase"<br>/codon_start=1<br>/product="large erk kinase"<br>/protein_id="BAA03537.1"<br>/db_xref="GI:285917"<br>/translation="LKLPRKREIFAIVAIKTLKSGYTEKORDFLSERSIMGQDPHPNVI<br>HLEGVTRSPVMIITEFMENGSLSDFLRNDQGFVYIQVGLRGLIAAGKRYLADNKK<br>YHNDLAAKRNILVNSNLVCKYSDGSLRFLSDPTLSALGKIPIRMTAPEALQ<br>YRKFTSSDWSVSTIVMEVMSYGERYHMTNDVYNALIDYRILPPMDCPALHQ<br>LMLDCKODRNRHRRFQIVTMTLDMKRNPSILKMAPLSSGIMPLDRTIDPTYSFS<br>NTVDWIKAIKMGQKESFANAGFTSPDVVSQMMEDILRQVTLAGHOKKILNSIOV<br>MRAQNNIOQSEV"<br>94..95<br>/gene="large erk"<br>/citation=[1]<br>/replace="gc"<br>220..225<br>/gene="large erk"<br>/citation=[1]<br>/replace="gtaggg" |      |
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VERSION AL512444.6 GI:12192913
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 181529)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 13, 2001 this sequence version replaced gi:12044686.
COMMENT

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----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA69E9
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 178625 bases at least Q40
Consensus quality: 179440 bases at least Q30
Consensus quality: 180200 bases at least Q20
Insert size: 180829; sum-of-contrigs
Insert size: 174363; 7.5% error; agarose-fp
Quality coverage: 6.77x in Q20 bases; sum-of-contrigs Quality
coverage: 7.07x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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12368 12467: gap of 100 bp
12468 20480: contrig of 8013 bp in length
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20581 23242: contrig of 2662 bp in length
23243 23342: gap of 100 bp
23343 88023: contrig of 64681 bp in length
88024 83123: gap of 100 bp
88124 102351: contrig of 14228 bp in length
102352 102451: gap of 100 bp
102452 117171: contrig of 14720 bp in length
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OY 144 CAACGCTTTGAGTCAAGCAAGCAACTGGCTACGACCAAGTTTATCCGCGCCCTGTG 203  
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 DB 39718 CAACGCTTTGAGTCAAGCAAGCAACTGGCTACGACCAAGTTTATCCGCGCCCTGTG 39659  
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OY 204 GGGCCACCGCATCCACGTGAGATGAAAGTTTTCGTCGCTGACCTGACAGCATCCCGAG 263  
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 DB 39658 GGGCCACCGCATCCACGTGAGATGAAAGTTTTCGTCGCTGACCTGACAGCATCCCGAG 39599  
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OY 264 CGTGGCTGGCTCCGTCGAAGAGAGACCTTCAACCTCTATTAGAGGCTGACTTTGACTC 323  
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OY 684 CGGGGACGCGAGTGGCTGTCGCCATCGGGGCTGTCATGTGCAAGCAAGGCTTGGAGGC 743  
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 DB 39178 CGGGGACGCGAGTGGCTGTCGCCATCGGGGCTGTCATGTGCAAGCAAGGCTTGGAGGC 39119  
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 AC013611 AC013611.3 GI:7341870  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 171553)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 TITLE  
 JOURNAL  
 COMMENT  
 Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 30, 2000 this sequence version replaced g1:6532099.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www.seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L3093  
 Center clone name: 10\_K\_8  
 ----- Summary Statistics  
 Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 165779 bases at least Q40  
 Consensus quality: 168407 bases at least Q30  
 Consensus quality: 169490 bases at least Q20  
 Insert size: 16900; agarose-fp  
 Insert size: 17053; sum-of-ctrls  
 Quality coverage: 5.5 in Q20 bases; agarose-fp  
 Quality coverage: 5.4 in Q20 bases; sum-of-ctrls  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 2990: contig of 2990 bp in length  
 \* 2991 3090: gap of 100 bp  
 \* 3091 7743: contig of 4653 bp in length  
 \* 7744 7843: gap of 100 bp  
 \* 7844 12243: contig of 4400 bp in length  
 \* 12244 12343: gap of 100 bp  
 \* 12344 17166: contig of 4823 bp in length  
 \* 17167 17266: gap of 100 bp  
 \* 17267 24222: contig of 6956 bp in length  
 \* 24223 24323: gap of 100 bp  
 \* 24323 33192: contig of 8870 bp in length  
 \* 33193 33292: gap of 100 bp  
 \* 33293 51470: contig of 18178 bp in length  
 \* 51471 51570: gap of 100 bp  
 \* 51571 72899: contig of 21329 bp in length  
 \* 72900 72999: gap of 100 bp  
 \* 73000 91876: contig of 18877 bp in length  
 \* 91877 91976: gap of 100 bp  
 \* 91977 128638: contig of 36662 bp in length  
 \* 128639 128738: gap of 100 bp  
 \* 128739 171553: contig of 42815 bp in length.  
 \* Location/Qualifiers  
 1. 171553

REFERENCE  
 AUTHORS  
 2 (bases 1 to 171553)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collumore, A.,  
 Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
 Ferrelira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D.,  
 Galagan, J., Gardyna, S., Grant, G., Haeos, B., Heaford, A., Horon, L.,  
 Howland, J., Johnson, R., Jones, C., Kann, L., Karatis, A., Klein, J.,  
 Lehoczy, J., Liu, C., Locke, K., Macdonald, P., Margulis, N.,  
 McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
 Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,  
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Tjirell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
 Wyman, D., Ye, W., J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 30, 2000 this sequence version replaced g1:6532099.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www.seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L3093  
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 Consensus quality: 169490 bases at least Q20  
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 Quality coverage: 5.5 in Q20 bases; agarose-fp  
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 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 2990: contig of 2990 bp in length  
 \* 2991 3090: gap of 100 bp  
 \* 3091 7743: contig of 4653 bp in length  
 \* 7744 7843: gap of 100 bp  
 \* 7844 12243: contig of 4400 bp in length  
 \* 12244 12343: gap of 100 bp  
 \* 12344 17166: contig of 4823 bp in length  
 \* 17167 17266: gap of 100 bp  
 \* 17267 24222: contig of 6956 bp in length  
 \* 24223 24323: gap of 100 bp  
 \* 24323 33192: contig of 8870 bp in length  
 \* 33193 33292: gap of 100 bp  
 \* 33293 51470: contig of 18178 bp in length  
 \* 51471 51570: gap of 100 bp  
 \* 51571 72899: contig of 21329 bp in length  
 \* 72900 72999: gap of 100 bp  
 \* 73000 91876: contig of 18877 bp in length  
 \* 91877 91976: gap of 100 bp  
 \* 91977 128638: contig of 36662 bp in length  
 \* 128639 128738: gap of 100 bp  
 \* 128739 171553: contig of 42815 bp in length.  
 \* Location/Qualifiers  
 1. 171553

FEATURES  
 source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-10X8"
/clone_lib="RPCT-11 Human Male BAC"
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  7844..12243
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  12344..17166
misc_feature
  /note="assembly_fragment"
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  vector_side:right"
  17267..24222
misc_feature
  /note="assembly_fragment"
  24323..33192
misc_feature
  /note="assembly_fragment"
  33293..51470
misc_feature
  /note="assembly_fragment"
  clone_end:T7
  vector_side:left"
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misc_feature
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  /note="assembly_fragment"
  91977..128638
misc_feature
  /note="assembly_fragment"
  128739..171553
misc_feature
  /note="assembly_fragment"
BASE COUNT 41218 a 43858 c 43894 g 41573 t 1010 others
ORIGIN

```

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 84 GTGGGAAGAGGTGATGCTGACATGAGAACATGACACGATCCGACGTACAGGTGTG 143
    |||||||
Db 145073 GTGGGAAGAGGTGATGCTGACATGAGAACATGACACGATCCGACGTACAGGTGTG 145014

QY 144 CAACGTGTGTGAGCAAGCCAGAACAACTGGCTACGACCAATTTATCCGGCCGCTGG 203
    |||||||
Db 145013 CAACGTGTGTGAGCAAGCCAGAACAACTGGCTACGACCAATTTATCCGGCCGCTGG 144954

QY 204 GGCCCAACCCGATCCACGTGAGATGAAGTTTGGTGGCTGACTGACGACATCCCGAG 263
    |||||||
Db 144953 GGCCCAACCCGATCCACGTGAGATGAAGTTTGGTGGCTGACTGACGACATCCCGAG 144894

QY 264 CGTGCTGGCTCTCTGCAAGAGACCTTCAACCTCTATTACTATGAGGCTGACTTGTACTC 323
    |||||||
Db 144893 CGTGCTGGCTCTCTGCAAGAGACCTTCAACCTCTATTACTATGAGGCTGACTTGTACTC 144834

QY 324 GGCCCAACGATCTCCCAACTGATGAGATTCATGGGTGAAGTGAATTCATTCG 383
    |||||||
Db 144833 GGCCCAACGATCTCCCAACTGATGAGATTCATGGGTGAAGTGAATTCATTCG 144774

QY 384 AGCCGACGAGAGCTTCTCCAGGTGAGACTGGGTGGCCGCTCATGAAATCAACACCGA 443
    |||||||
Db 144773 AGCCGACGAGAGCTTCTCCAGGTGAGACTGGGTGGCCGCTCATGAAATCAACACCGA 144714

QY 444 GGTCGAGACCTTGGACACCTGTGTCCCGACGGGCTTCTACCTGGCCCTTCAGAGACTANGG 503
    |||||||
Db 144713 GGTCGAGACCTTGGACACCTGTGTCCCGACGGGCTTCTACCTGGCCCTTCAGAGACTANGG 144654

QY 504 CGGCTGACATGCTCCATGATGGCGGTGCTTCTTACCCAGTGGCCCGGATATCA 563
    |||||||
Db 144653 CGGCTGACATGCTCCATGATGGCGGTGCTTCTTACCCAGTGGCCCGGATATCA 144594

QY 564 GAATGGCGCATCTTCCAGGAAACCTGTGCGGGGCTGAGACATGCTGCTGCTGC 623
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Db 144593 GAATGGCGCATCTTCCAGGAAACCTGTGCGGGGCTGAGACATGCTGCTGCTGC 144534

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QY 624 CCGGGACGATGCTATCCCAATGCGGAAGAGTGATGATCCCATCAAGCTCTACTGTAA 683
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Db 144533 CCGGGACGATGCTATCCCAATGCGGAAGAGTGATGATCCCATCAAGCTCTACTGTAA 144474

QY 684 CCGGGACGCGGAGTGGCTGGTGGCCATCGGGCGCTGATGTGCAAGCAGGCTTCAGGC 743
    |||||||
Db 144473 CCGGGACGCGGAGTGGCTGGTGGCCATCGGGCGCTGATGTGCAAGCAGGCTTCAGGC 144414

QY 744 CGTTGAGATGCGACCGCTGCGGAGGT 771
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Db 144413 CGTTGAGATGCGACCGCTGCGGAGGT 144386

RESULT 13
AL157403/c
LOCUS
DEFINITION
  AL157403 111026 bp DNA HTG 23-JAN-2001
  Homo sapiens chromosome 1 clone RP5-1158110 map p22.3-31.2, ***
  SEQUENCING IN PROGRESS ***, 13 unordered pieces.
ACCESSION
  AL157403
KEYWORDS
  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
  1 (bases 1 to 111026)
REFERENCE
  Pavlitt,R.
  Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
  CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
  requests: clonerequest@sanger.ac.uk
  On Aug 12, 2000 this sequence version replaced gi:9212375.
COMMENT
  ----- Genome Center
  Center: Sanger Centre
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: humquery@sanger.ac.uk
  ----- Project Information
  Center project name: d1158110
  ----- Summary Statistics
  Assembly program: XGAP4; version 4.5
  Sequencing vector: plasmid; 108752; 100% of reads
  Chemistry: Dye-terminator ABI; 0% of reads
  Chemistry: Dye-terminator Big Dye; 99% of reads
  Consensus quality: 10565 bases at least Q40
  Consensus quality: 107614 bases at least Q30
  Insert size: 109626; sum-of-contrigs
  Quality coverage: 3.50x in Q20 bases; sum-of-contrigs
  -----
  * NOTE: This is a 'working draft' sequence. It currently
  * consists of 13 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contrigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
  1 7499: contig of 7499 bp in length
  * 7500 7599: gap of 100 bp
  * 7600 10440: contig of 2841 bp in length
  * 10441 10540: gap of 100 bp
  * 10541 17763: contig of 7223 bp in length
  * 17764 17863: gap of 100 bp
  * 17864 33875: contig of 16012 bp in length
  * 33876 33975: gap of 100 bp
  * 33976 43661: contig of 9686 bp in length
  * 43662 43761: gap of 100 bp
  * 43762 52351: contig of 8590 bp in length
  * 52352 52451: gap of 100 bp
  * 52452 57434: contig of 4983 bp in length
  * 57435 57534: gap of 100 bp

```

```

* 57535 64699: contig of 7165 bp in length
* 64700 64799: gap of 100 bp
* 64800 67779: contig of 2980 bp in length
* 67800 67879: gap of 100 bp
* 67880 75753: contig of 7874 bp in length
* 75754 75853: gap of 100 bp
* 75854 84741: contig of 8888 bp in length
* 84742 84841: gap of 100 bp
* 84842 101025: contig of 16184 bp in length
* 101026 101125: gap of 100 bp
* 101126 111026: contig of 9901 bp in length.

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FEATURES  
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1. .111026  
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/db\_xref="taxon:9606"  
/chromosome="1"  
/map="p22.3-31.2"  
/clone="RP5-1158110"  
/clone\_lib="RPC1-5"  
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clone\_end:SP6  
vector\_side:left"  
7600. .10440  
/note="assembly\_fragment:00467  
fragment\_chain:1"  
10541. .17763  
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/note="assembly\_fragment:00050"  
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/note="assembly\_fragment:00599"  
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84842. .101025  
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/note="assembly\_fragment:00426  
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clone\_end:77  
vector\_side:right"

BASE COUNT 27906 a 27001 c 26072 g 28846 t 1201 others  
ORIGIN

Query Match 8.5%; Score 251; DB 79; Length 111026;  
Best Local Similarity 100.0%; Pred. No. 6.6e-132;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1838 CAGGGAGTTTGGCAGGCTCTGACCTGACCTGACGAGCAAGAGAGATCT 1897  
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DB 84408 CAGGGAGTTTGGCAGGCTCTGACCTGACCTGACGAGCAAGAGAGATCT 84349  
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OY 1898 TTGTGGCCATCAAGAGCTCAAGTCGGGCTACAGGAGAGAGAGAGAGAGAGATCT 1957  
|||||  
DB 84348 TTGTGGCCATCAAGAGCTCAAGTCGGGCTACAGGAGAGAGAGAGAGAGAGATCT 84289  
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OY 1958 GCGAAGCCTCCATCATCGGCGCAGTTGACCATCCCAACGTCATCCACCTGGAGGCTCG 2017  
|||||  
DB 84288 GCGAAGCCTCCATCATCGGCGCAGTTGACCATCCCAACGTCATCCACCTGGAGGCTCG 84229  
|||||  
OY 2018 TGACCAAGAGCAGCCTGTGTGATCATCACCAGTTCATGAGATGCTCCTGACT 2077  
|||||  
DB 84228 TGACCAAGAGCAGCCTGTGTGATCATCACCAGTTCATGAGATGCTCCTGACT 84169  
|||||  
OY 2078 CCTTTCCTCCGG 2088  
|||||  
DB 84168 CCTTTCCTCCGG 84158  
|||||

## RESULT 14

HS74M1 113956 bp DNA PRI 27-SEP-2000  
LOCUS Human DNA sequence from clone RPL-74M1 on chromosome 1p34.3-36.13  
DEFINITION Contains the EPHB2 gene for a protein tyrosine kinase. Contains  
ESTs, GSSs, STS and a CpG island, complete sequence.

## ACCESSION

AL035704.9 GI:6165330  
HTG: Cpg island; EPHB2; tyrosine kinase.

## VERSION

human.

## KEYWORDS

human.

## SOURCE

human.

## ORGANISM

human.

## REFERENCE

1 (bases 1 to 113956)

## AUTHORS

Baggaley,C.

## TITLE

Direct Submission

## COMMENT

Submitted (27-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Oct 31, 1999 this sequence version replaced g1:6065897.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chrl  
RPL-74M1 is from the library RPC1-1 constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong. For further  
details see http://bacpac.med.buffalo.edu/  
VECTOR: pCYPAC2  
This sequence is the entire insert of clone RPL-74M1.

## FEATURES

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/clone\_lib="RPC1-1"  
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527. .624  
/note="MIR repeat: matches 47. .151 of consensus"  
804. .861  
/note="MIR repeat: matches 88. .145 of consensus"

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/!note="AluSx repeat: matches 1. .286 of consensus"
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/!note="LIMBS repeat: matches 6129. .6172 of consensus"
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30269. .30462,32331. .32486,33349. .35193)
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/!note="match: CDNAS: Em:AF025304 Em:X75208 Em:AF037331
Em:AF037332 Em:AF03733 Em:IA0636 Em:U14164 Em:IA620 Em:IA6325
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Em:IA621 Em:IA1939 Em:Z19110 Em:L25890 Em:X76011
Em:D37827 Em:M59814 Em:E09831 Em:Z19061 Em:U11493
Em:U23783 Em:Z49086 Em:U06834 Em:X65138 Em:S57168
Em:U07695 Em:Z19059 Em:AJ005029 Em:X13411 Em:D38174
Em:Z49085 Em:E11714 Em:AJ236868 Em:AB025542 Em:M59371
Em:U07634 Em:D14717 Em:AJ005026 Em:X76010 Em:X78339
Em:Z19058 Em:AB025543 Em:U03910 Em:X76012 Em:U89379
Em:M83941 Em:AJ005030 Em:M68514 Em:AJ236867 Em:X60380
Em:AB040892 Em:X59290 Em:X15345 Em:L14782 Em:X52882
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Em:AF216799 Em:AF237766
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Em:AI940301 Em:AW374328 Em:AA341538 Em:T04965 Em:AW374262
Em:AA298037 Em:AA569391 Em:AI742214 Em:AW662549
Em:AA52367 Em:AI08197 Em:W96473 Em:W96506 Em:AI809403
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Em:W76439 Em:AI702993 Em:AI476586 Em:AM365103 Em:AA570007
Em:AM168439 Em:AI344182 Em:AI911816 Em:AI345870
Em:AM374261 Em:AI61293 Em:AA524449 Em:AM582672
Em:AA505550 Em:AA505559 Em:AA515992"
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30269. .30462,32331. .32486,33349. .33451,33545. .35193)
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Em:L36643 Em:X76011 Em:X75208 Em:AF026039 Em:IA3620
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Em:AF037331 Em:M59814 Em:E09831 Em:Z19061 Em:U23783
Em:U249086 Em:U11493 Em:E11714 Em:Z19059 Em:X65138
Em:U06834 Em:X13411 Em:D38174 Em:AJ005029 Em:Z49085
Em:S57168 Em:U07695 Em:D14717 Em:U07634 Em:AJ005026
Em:AB025542 Em:M59371 Em:X76010 Em:X78339 Em:AJ226868
Em:U03910 Em:U89379 Em:M68514 Em:M83941 Em:AJ005030
Em:Z19058 Em:X76012 Em:AB025543 Em:AJ236867 Em:X60380
Em:X59290 Em:AB040892 Em:X15345 Em:L14782 Em:L14445
Em:AF041811 Em:L14823 Em:X52882 Em:L14446 Em:L14447
Em:AF176552 Em:AF216772 Em:AF216773 Em:AF245114
Em:AF216799 Em:AF237766
match: ESTS: Em:AI940384 Em:AM062316 Em:AM51853 Em:M85491
Em:AI940301 Em:AW374261 Em:AA341538 Em:IA620 Em:IA6325
Em:AA298037 Em:AA569391 Em:AA341538 Em:IA620 Em:IA6325
Em:AA52367 Em:AI038197 Em:W96473 Em:W96506 Em:IA809403
Em:AA505599 Em:AA387292 Em:AA573757 Em:AI216739
Em:AI739658 Em:W73189 Em:AI445236 Em:AA622626 Em:AI268257
Em:AM168402 Em:AA505740 Em:AA552072 Em:W27292 Em:AI345860
Em:W76439 Em:AI702993 Em:AI476586 Em:AM365103 Em:AA570007
Em:AM168439 Em:AI344182 Em:AI911816 Em:AI345870
Em:AA161293 Em:AA524449 Em:AM582672 Em:AA505550
Em:AA505559 Em:AA515992 Em:AI742214"
/!evidence=not_experimental
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/!product="dj74M1.1.2 (tyrosine kinase isoform 2)"
2246. .35193
/!gene="EPHB2"
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/!note="continues in dj61A9 (AL035703), gene dj61A9.1
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Sw:Q90344 Tr:041569 Sw:P09759 Sw:P54762 Tr:007494
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| Db | 26534 | CAGGGGAACTTTGGGAGGCTCTGCAGTGGCCACCTGAAAGCTCCAGGCAAGAGAGATCT  | 26653 |
| OY | 1988  | TTGTGGCCATCAAGACGCTCAAGTCGGGCTACACGGAGACAGCGCGCGGACTTCCTGA   | 1957  |
| Db | 26654 | TTGTGGCCATCAAGACGCTCAAGTCGGGCTACACGGAGAGACAGCGCGCGGACTTCCTGA | 26713 |
| OY | 1958  | GCGAAGCCTTCATGATGGCGCAGTTGCACCATCCCAACGTCATCCACTTGAAGGTTGTG  | 2017  |
| Db | 26714 | GCGAAGCCTTCATGATGGCGCAGTTGCACCATCCCAACGTCATCCACTTGAAGGTTGTG  | 26773 |
| OY | 2018  | TGACCAAGACGACACCTGTGATGATCATCAACCGATTCATGAGAAATGGCTCCCTGGACT | 2077  |
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| OY | 2078  | CGTTTCCTCCG  | 2088  |
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|------------|---|
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| LOCUS      | AC067727 149709 bp DNA HTG 06-SEP-2000  |
| DEFINITION | Homo sapiens chromosome 3 clone RP11-6916, WORKING DRAFT SEQUENCE<br>22 unordered pieces. |
| ACCESSION  | AC067727  |
| VERSION    | AC067727.5 GI:9438548   |
| KEYWORDS   | HTG; HTGS_PHASE1; HTGS_DRAFT.   |
| SOURCE     | human.  |
| ORGANISM   | Homo sapiens  |

| TITLE             | JOURNAL     | REFERENCE             | AUTHORS      | TITLE             | JOURNAL  |
|-------------------|-------------|-----------------------|--------------|-------------------|--|
| Direct Submission | Unpublished | 2 (bases 1 to 149709) | Worley, K.C. | Direct Submission | Submitted (27-APR-2000)  |
|                   |             |                       |              |                   | Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |
|                   |             |                       |              |                   | On July 25, 2000 this sequence version replaced g1:8699853.  |
| COMMENT           |             |                       |              |                   |  |

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc.help@bcm.tmc.edu  
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Project Information  
Center project name: HAXB  
Center clone name: RP11-6916  
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Summary Statistics  
Sequencing Summary: M13:L080821

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Chemistry: Dye-Primer Bodyfip: 47% of reads
Chemistry: Dye-terminator Big Dye: 53% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 137058 bases at least Q40
Consensus quality: 144887 bases at least Q30
Consensus quality: 149602 bases at least Q20
Estimated insert size: 142903: sum-of-configs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.4x in Q20 bases; sum-of-configs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 32212: contig of 32212 bp in length
* 32213 32312: gap of unknown length
* 32313 31391: contig of 19079 bp in length
* 51392 51491: gap of unknown length
* 51492 66100: contig of 14609 bp in length
* 66101 66200: gap of unknown length
* 66201 77037: contig of 10837 bp in length
* 77038 77137: gap of unknown length
* 77138 85439: contig of 8302 bp in length
* 85440 85539: gap of unknown length
* 85540 92202: contig of 6663 bp in length
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* 100919 100918: contig of 8616 bp in length
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* 107378 107477: gap of unknown length
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Best Local Similarity 100.0%; Pred. No. 6.5e-132;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 47714 CAGGGAGTTTGGCGAGTCTGCACTGCGCACCTGAAGCTGCCAGGCAAGAGAGATCT 47655  
|||||

OY 1898 TTGTGGCCATCAAGACGCTCAAGTGGGCTACACGAGAGAAAGCGCGGACTTCTCTGA 1957  
|||||  
Db 47654 TTGTGGCCATCAAGACGCTCAAGTGGGCTACACGAGAGAAAGCGCGGACTTCTCTGA 47595  
|||||

OY 1958 GCGAAGCCTTCATCATGGGCGAGTTGACCATCCCAACGTCATCCACCTGAGAGGTGTCG 2017  
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OY 2018 TGACCAAGACACACCTGTGATGATCATCACCGAGTTTCATGAGAAATGGCTCCCTGGACT 2077  
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Db 47534 TGACCAAGACACACCTGTGATGATCATCACCGAGTTTCATGAGAAATGGCTCCCTGGACT 47475  
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OY 2078 CCTTTCTCCGG 2088  
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Db 47474 CCTTTCTCCGG 47464  
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Job time: 10270 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 18:41:48 ; Search time 195.34 Seconds  
(without alignments)  
9521.064 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CCGCTCGCGCGCGCTGAGAGA.....CCAGGCCCGCGCCCTCTGCG 2962

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 730101 segs, 313950809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 2962  | 100.0       | 2962   | 16 AAT02946 | EPH-like receptor  |
| 2          | 2233  | 75.4        | 3949   | 21 AAA88549 | Human CASB616 CDNA |
| 3          | 1996  | 67.4        | 3768   | 21 AAA88548 | Human CASB616 CDNA |
| 4          | 1673  | 56.5        | 3151   | 21 AAA09322 | Human cancer assoc |
| 5          | 120   | 4.1         | 171    | 16 AAQ96250 | Partial DNA encodi |
| 6          | 85    | 2.9         | 381    | 14 AAQ60025 | Human brain expres |
| 7          | 48    | 1.6         | 3105   | 16 AAT07308 | Receptor tyrosine  |
| 8          | 48    | 1.6         | 3105   | 16 AAT84528 | Mouse Nuk tyrosine |
| 9          | 32    | 1.1         | 3776   | 16 AAQ90655 | EPH-related PTK Ce |
| 10         | 30    | 1.0         | 3751   | 15 AAQ62461 | Human embryonal Ki |
| 11         | 29    | 1.0         | 3133   | 16 AAQ90652 | EPH-related tyrosi |

|    |    |     |      |             |                    |
|----|----|-----|------|-------------|--------------------|
| 12 | 29 | 1.0 | 3592 | 20 AAV70208 | Rat receptor tyros |
| 13 | 29 | 1.0 | 4049 | 16 AAQ90660 | Eph-related PTK Ce |
| 14 | 29 | 1.0 | 4097 | 16 AAQ90657 | Eph-related PTK Ce |
| 15 | 26 | 0.9 | 1509 | 14 AAQ53470 | PTK gene Bl. Ratt  |
| 16 | 26 | 0.9 | 4281 | 14 AAQ53471 | elk CDNA. Rattus   |
| 17 | 25 | 0.8 | 39   | 16 AAT02951 | HEK5 extracellular |
| 18 | 25 | 0.8 | 81   | 13 AAQ30727 | Potential tyrosin  |
| 19 | 25 | 0.8 | 3546 | 16 AAQ90656 | Rat orphan tyrosin |
| 20 | 25 | 0.8 | 3546 | 16 AAQ90656 | Eph-related PTK Ce |
| 21 | 25 | 0.8 | 3591 | 16 AAQ90658 | Eph-related PTK Ce |
| 22 | 25 | 0.8 | 3591 | 16 AAQ90658 | HEK5 extracellular |
| 23 | 24 | 0.8 | 54   | 16 AAT02953 | Elk receptor signa |
| 24 | 24 | 0.8 | 3669 | 14 AAQ49757 | PTK gene HprtK5. H |
| 25 | 24 | 0.8 | 3669 | 16 AAT03099 | Protein tyrosine-k |
| 26 | 24 | 0.8 | 4290 | 16 AAQ92641 | Human non-differen |
| 27 | 24 | 0.8 | 4290 | 17 AAT42593 | Coding sequence fo |
| 28 | 24 | 0.8 | 4290 | 17 AAT18394 | Receptor type tyro |
| 29 | 24 | 0.8 | 4290 | 18 AAT51235 | Receptor type tyro |
| 30 | 23 | 0.8 | 171  | 19 AAV55890 | Receptor protein t |
| 31 | 23 | 0.8 | 171  | 20 AAV65312 | Receptor protein t |
| 32 | 23 | 0.8 | 2170 | 20 AA241307 | Human normal ovar  |
| 33 | 23 | 0.8 | 2982 | 16 AAQ90971 | Protein p140 CDNA  |
| 34 | 23 | 0.8 | 3056 | 16 AAQ90662 | Eph-related PTK Ce |
| 35 | 23 | 0.8 | 3059 | 16 AAQ90653 | Eph-related PTK Ce |
| 36 | 23 | 0.8 | 3125 | 16 AAQ90661 | Eph-related PTK Ce |
| 37 | 23 | 0.8 | 4027 | 16 AAQ90972 | Protein p140 CDNA  |
| 38 | 23 | 0.8 | 4027 | 16 AAQ90982 | Protein p140 CDNA  |
| 39 | 22 | 0.7 | 171  | 19 AAV55891 | Receptor protein t |
| 40 | 22 | 0.7 | 171  | 20 AAV65313 | Receptor protein t |
| 41 | 21 | 0.7 | 21   | 22 AAF97524 | Human gene single  |
| 42 | 21 | 0.7 | 21   | 22 AAF97526 | Human gene single  |
| 43 | 21 | 0.7 | 3162 | 16 AAT02947 | EPH-like receptor  |
| 44 | 20 | 0.7 | 171  | 19 AAV55896 | Receptor protein t |
| 45 | 20 | 0.7 | 171  | 20 AAV65318 | Receptor protein t |

ALIGNMENTS

|              |  |
|--------------|--|
| RESULT 1     |  |
| ID AAT02946  | standard; CDNA; 2962 BP.   |
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| AC           |  |
| XX           |  |
| DT           | 16-APR-1996 (first entry)  |
| XX           |  |
| DE           | EPH-like receptor protein tyrosine kinase HEK5 CDNA.             |
| XX           |  |
| KW           | EPH-like receptor protein tyrosine kinase; PTK; HEK5;            |
| KW           | human eph-like kinase; therapy; diagnosis; antibody; vector; ss. |
| XX           |  |
| OS           | Homo sapiens.  |
| XX           |  |
| FH           | Key  |
| FT           | CDS  |
| FT           | Location/Qualifiers  |
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| XX           | /*tag- a   |
| PN           | W09528484-A1.  |
| PD           | 26-OCT-1995.   |
| XX           |  |
| PF           | 14-APR-1995; 95WO-US04681.                                       |
| XX           |  |
| PR           | 15-APR-1994; 94US-0229509.                                       |
| XX           |  |
| PA           | (AMGE-) AMGEN INC.   |
| XX           |  |
| PI           | Fox GM, Jing S, Welcher AA;                                      |
| XX           |  |
| DR           | WPI: 1995-373799/48.   |
| XX           | P-PSDB; AAR85089.  |
| XX           |  |



PT New nucleic acid encoding Eph-like receptor tyrosine kinase(s)  
 PT and related vectors, host cells, proteins, antibodies etc., used  
 PT diagnostically and therapeutically to modulate receptor activation  
 PT or prodn.

PS Claim 1; Page 41-45; 133pp; English.

XX cDNAs (AA02946-49) coding for 4 novel human Eph-like receptor protein  
 CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (AR85089-92),  
 CC respectively, were isolated from a human foetal brain cDNA library using  
 CC a directed PCR approach with primers (see AA02960-61) based on conserved  
 CC regions of receptor PKTs and Eph-like receptor PKTs. HEK5, HEK7 and HEK8  
 CC show extensive homology to the catalytic domain of chicken Eph-like  
 CC receptors Cxk5, Cxk7 and Cxk8. HEK11 shows no homology to any known  
 CC Eph-like receptor. The isolated cDNAs are used for prodn. of  
 CC recombinant HEKs and chimeric receptors, in hybridisation assays, and  
 CC to detect abnormalities in HEK receptor genes.

SQ Sequence 2962 BP; 654 A; 914 C; 827 G; 567 T; 0 other;

Query Match 100.0%; Score 2962; DB 16; Length 2962;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 agatccgcacgtacacagtggtgcaacgtgttgagtcacagccagaactgtctacgg 180  
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Db 2941 ctccaagccccgccctctgc 2962

RESULT 2
AAA88549
ID AAA88549 standard; cDNA: 3949 BP.
XX
AC AAA88549:
XX
DT 22-JAN-2001 (first entry)
XX
DE Human CASB616 cDNA.
XX
KW CASB616; EPHB2; ERK; EPH3; EPH3.3; DRT; HEK5; EPHB2V;
KW receptor protein tyrosine kinase; human; antigen; colon cancer;
KW ovary cancer; tumour; autoimmune disease; vaccine; gene therapy;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 26..3193
FT FT /*tag= a
XX
XX MO200053216-A2.
XX
PD 14-SEP-2000.
XX
PE 28-FEB-2000; 2000WO-EP01587.
XX
PR 05-MAR-1999; 99GB-0005124.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Vinals De Bassols YC;
XX
XX WPI: 2000-587384/55.
DR P-PSDB: AAB19591.
XX
PT Vaccine composition for treating ovarian and colon cancer, comprises
PI CASB616 polypeptides, polynucleotides or antigen presenting cells
XX expressing the polypeptides
XX
PS Claim 3; Page 41-42; 57pp; English.
XX
CC The present sequence is that of cDNA coding for human CASB616 (see
CC AAB19591), a member of the EPH and EPH-related family of receptor
CC protein tyrosine kinases. CASB616 is also known as EPHB2, ERK,
CC EPH3, EPH3.3, DRT, HEK5 and EPHB2V. CASB616 polypeptides and
CC polynucleotides are important immunogens for specific prophylactic
CC or therapeutic immunization against tumours, especially colon
CC cancer (claimed) and ovarian cancer. They are specifically
CC expressed or highly over-expressed in tumours compared to normal
CC cells and can thus be targeted by antigen-specific immune
CC mechanisms leading to destruction of the tumour cells. They can
CC also be used to diagnose the occurrence of tumour cells. Their
CC inappropriate expression can also cause an induction of autoimmune
CC responses, which can be corrected through vaccination using the
CC CASB616 polypeptides or polynucleotides.
XX
SQ Sequence 3949 BP; 934 A; 1142 C; 1105 G; 768 T; 0 other;

Query Match 75.4%; Score 2233; DB 21; Length 3949;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

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QY 2392 ATTGTATGTGGGAGTGTGCTATGGGAGCGGCTTATGGGCAATGACCAACAG 2451  
|||||  
Db 2547 atgtcatgtggaggtgagtgctccatgaggagcgccctactggaatgaaccaacag 2606  
QY 2452 GATGTATCAATGCAATTGAGCAGGACTATGCGTGCACACGCCCATGAGTGCAGCAGC 2511  
|||||  
Db 2607 gatgtatcaatgaatctgagcagatcatgctgcgcaacgcccatagtacgctcgagc 2666  
QY 2512 GCCCTGACCACTATGCTGTGACTGTGTGGCAAGAGACCGCAACCCAGCCCAAGTTC 2571  
|||||  
Db 2667 gccctgacccaactatgctgagctgtgtgcaagaagacgcaacacagcccaagcttc 2726  
QY 2572 GGCCAAAATTGTCAACAGCTAGACAGATGATCCGCAATCCCAAGCTCAAAAGCCATG 2631  
|||||  
Db 2727 ggcacaattgtcaacaagctagacaagaatgacatcgcaatcccaagcctcaaaagccatg 2786  
QY 2632 GCGCCCTCTCTCTGAGCATCAACCTGCCGCTGTGAGCCGACAGATCCCGCATACAC 2691  
|||||

Db 2787 ggcgccctctctctctgcatcaaacctgcgctgtagccgcaacatcccgactaacac 2846  
Oy 2692 AGCTTAAACGGTGGAGCGATGGCTGAGGCCATCAAGATGGGGCACTACAGAGAGC 2751  
Db 2647 agcttcaacagtgagcagcgtgtagcagcattcaagatgggagcagtaacaagagagc 2906  
Oy 2752 TTCCCAATGCGCGCTTCCACCTCTTTAGCTGCTGTCTCAGATGATGAGAGACATT 2811  
Db 2607 ttgcgaatgctcgcgtctcaactctcttgaagctgctgctcaagatgtagagagacat 2966  
Oy 2612 CTCGGGTTGGGCTCACTTTGGCTGGCCACCAAGAAAAATCCGACAGTATCCAGTG 2871  
Db 2667 ctccgggtctggcctcactcttgctgcacacagaaaaatccctgaaacagatccagtg 3036  
Oy 2672 ATGGGGGCGCATGAACAGATTGAGTGTGGAGTTTGACATTCACCTGCGGCT 2931  
Db 3027 atgggggagcagagaaacagatcagctgtagaggttgcacatcaacctgctcggt 3086  
Oy 2932 CACCTTCTCTCAAGCCGCCGCCCTCTGTC 2962  
Db 3087 cactctctcctcaagcccgccctctgc 3117

RESULT 4  
ID AAA09322 standard; DNA: 3151 BP.  
XX  
AC AAA09322;  
XX  
Dt 10-AUG-2000 (first entry)  
XX  
De Human cancer associated antigen precursor DNA, clone NY-REN-47.  
XX  
Km renal cancer; cancer associated antigen precursor; diagnosis;  
Km cytosolic; ERK tyrosine kinase; ss.  
XX  
Os Homo sapiens.  
XX  
Pn W0200020587-A2.  
PD 13-Apr-2000.  
XX  
Pf 04-OCT-1999; 99WO-US22873.  
XX  
Pr 05-OCT-1998; 98US-0166300.  
Pr 05-OCT-1998; 98US-0166350.  
XX  
Pa (LUDM-) LUDWIG INST CANCER RES.  
XX  
Pi Obata Y, Gout I, Tureci O, Sahin U, Pfreundschuh M, Scanlan MJ;  
Pi Stockert E, Chen Y, Old LJ, Jager E, Knuth A;  
Dr WPI: 2000-303774/26.  
XX  
Pt Preventing, diagnosing and/or treating disorders associated with  
Pt abnormal expression of human cancer associated antigens  
XX  
Ps Claim 57; Page 93-94; 121pp; English.  
XX  
Cc AAA09321-45 were isolated by SEREX screening from a renal cancer  
Cc cell line 1973/10.4. Homology searching revealed that these clones  
Cc correspond to known genes. The present sequence has identity with the  
Cc ERK tyrosine kinase gene. The genes encode cancer associated antigen  
Cc precursors. These gene products are useful in methods for preventing,  
Cc diagnosing and/or treating disorders, especially cancer, associated with  
Cc abnormal expression of human cancer associated antigens. The method  
Cc comprises contacting a sample from a subject with an agent that  
Cc specifically binds to the nucleic acid molecule or expression product  
Cc (or fragment) complexed with a human leukocyte antigen (HLA) molecule  
Cc and determining the interaction between the agent and the nucleic acid  
Cc molecule or the expression product as a determination of the disorder.  
S0 Sequence 3151 BP; 707 A; 974 C; 874 G; 596 T; 0 other;

Query Match 56.5%; Score 1673; DB 21; Length 3151;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2933; Conservative 0; Mismatches 12; Indels 9; Gaps 2;  
Oy 18 AGAAACGCTAATGATCTCCATACAGGAGCTGTGAGCTGGGCTGATGCTCTCC 77  
Db 66 agaaacgctaattgactccactcaacagcagctgtagctgagctggtctgagctctcc 125  
Oy 78 ATCAGGTGGGAGAGAGGTGAGTGGCTACGATGAGAAATGAAACGATCCGACGTACA 137  
Db 126 atcaggtgggagagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 185  
Oy 138 GGTGTCAACGCTGTTTGTAGTCAAGCCAGAACACTGGCTACGACCAAGTTTATCCGGC 197  
Db 186 ggtgtcaacgctgtttagtcaagccagaaacactggtacagccagagttatccggcg 245  
Oy 198 CCGTGGGGCCACCGCATCCACGTGAGATGAACTTTGGTGGTGTGACGACACAT 257  
Db 246 ccgtggggccacccgcatccacgtgagatgaaatttgcgtgtagctgtagcagcat 305  
Oy 258 CCCAGGCTGCTGGGCTGCTGCAAGAGAGACCTTCACCTTATATGAGGCTGACTT 317  
Db 306 cccaggtgctggtggtctctgcaagagagacccatcaactcatatcaatgaggtgactc 365  
Oy 318 TGACTCGGCGCACAGACTTCCCACTGGATGAGATGAGATTCATGAGTGAAGTGATAC 377  
Db 366 tgactcggcgcaacagacactcccaactgga tggagatccatccatcggtgaggtgagta 425  
Oy 378 CATTGACAGCCGACAGAGACTTTCCTCCAGTGGAGCTGGGTGGCGGCTGATGAATCAA 437  
Db 426 catlgacagccagagagctctcccaagtgagctgggtgagcgtgcaagaaatcaa 485  
Oy 438 CACGAGGTGGGAGGCTTCGAGACTGTGTCCGACGAGGCGCTTACCTGGGCTTCAAGA 497  
Db 486 caccgaggtggagagcttggaacctggtgccgagcgctctcaactggtcccgga 545  
Oy 498 CTATGGGCGCTGATGTCCATCATCGCGTGCGTGTCTTACCGCAAGTCCCGCAT 557  
Db 546 ctatggcgctgcatgtctcccatcgcgtgctggtcttcaacgcaagtgccccgat 605  
Oy 558 CATCCAGATGGCGCATCTTCCAGAAACCTGTCCGGGGCTGAGAGCAATGGCTGCT 617  
Db 606 catccagatggcgcatcttccagaaacccgtgcggggctgagagcaatcgcggtc 665  
Oy 618 GCGTGGCGGCGAGCTGCATCGCAATCGGAAGAGGTGATGTACCATCAAGCTCTA 677  
Db 666 gctggtggcgagcgtgcatcgcgaatcggaagagtgagtgatccatccaaactcta 725  
Oy 678 CTGTAACGGGAGCGGAGTGGCTGTGTCCTCATCGGCGCTGATGTGCAAGAGCTT 737  
Db 726 ctgtaacgggagcgcgagtggtgctggtccatcggtgcgctgagtgagtgagtgag 785  
Oy 738 CGAGGCGCTTGAAGATGGCACCCTGTCCGAGGTTGTCCATCTGGGATTTCAAGGCCAA 797  
Db 786 cgaggtcggtgagatggcaccgtctgcgaggtgtgtccatctggtgacttcaaggccaa 845  
Oy 798 CCAAGGATGAGGCGCTTACCCACTGTCCCATCAACAGCCGACACTTGTGAAGGGC 857  
Db 846 ccaaggatgagcgtgtgactccactgtcccatcaacagccggaactcttgaaagggc 905  
Oy 858 CACCACTGTGTCTGCGCAATGGCTACTACAGACAGACTGTGACCCCTGGACATGCC 917  
Db 906 caccacgtgtctgctcgcaatgtctactaaagcagaactggaaccccgagatgccc 965  
Oy 918 CTGCACACCATCCCTTCGCGGCCCGAGGCTGATTTCCAGTGTGACGTGACTCCCT 977  
Db 966 ctgcaacacatccctcccgcccgccaggtgaggtatctccagtgcaatgagacccctc 1025  
Oy 978 CATGCTGAGTGAACCCCTCCCGGAGCTCGGAGGCGGAGAGACCTGCTTACACAT 1037  
Db 1026 catgctgagtgagacccctcccgagactccggaggtcgagagagcctcgtctacaacat 1085



QY 1038 CATCTGCAAGAGCTGTGGCTCGGGCCGGGGTGCCTGCACCCCGCTGCGGGGACAAATGTACA 1097  
 |||||||  
 Db 1086 catctgaagagctgtgtcctcgagccgggtgtcctgtcacccgcgtcggggaacaattgtaca 1145  
 QY 1098 GTACGACACCGCAGAGTAAAGCCCTGACACGACCAACGATTTACATCATGTACCTGCTGGC 1157  
 |||||||  
 Db 1146 gtacgacacacgacagctgaagcctgtacagcagcagcattacatcagtgacctgtcgtgc 1205  
 QY 1158 CCACACCACTAGACCTTCCAGATCCAGGCTGTGAAGCGGGTTTACTGACAGAGCCCTT 1217  
 |||||||  
 Db 1206 ccaacacccagtaaacctctgtgagatccaggtctgtgaagcggttactgtacagagccctt 1265  
 QY 1218 CTGCGCTCAGTTGGCTCTGTGTGAACATCACACCAACAGGAGCTTCATCGGCAAGTTC 1277  
 |||||||  
 Db 1266 ctgcgcctcagctcgcctctgtgaacatcaccaacacagcagctccatccgtcaggtgc 1325  
 QY 1278 CATCATGCAATCAGGTAGCGCCGACCGGTGGACAGCATTTACCTGTGCTGCTCCAGCCGGA 1337  
 |||||||  
 Db 1326 catcatgtcatcaggtgagccgacccgtgtgacagcattacccctgtgtgtccagccaga 1385  
 QY 1338 CCAGCCCAATGGCGGTATCCTGTGACTATGAGTGCAGTACTATGAGA--AGGAGCTCAG 1394  
 |||||||  
 Db 1386 ccagcccaatggtgtgtatctgtgactatgagctgcagctactatgtagaagcagagctcag 1445  
 QY 1395 TGAATCAACACGCGACAGCCATAAAAAAGCCCAACACAGGTAC-----GGGCTCAA 1448  
 |||||||  
 Db 1446 tgaatacaacgacacagccataaaagcccaacaacgctacagctgtgagggcctca 1505  
 QY 1449 AGCGGCGCATTTATGTCTTCCAGGTGGCGGACGACACTGTGTGGAGGCTACGGGGGCTA 1508  
 |||||||  
 Db 1506 agccggcgcatctatgtcttccaggtgtgcagcagccgtgtgaggtctacagggcctta 1565  
 QY 1509 CACGCGCAAGATGATCTTACATCCAGACATGACAGAGCGGAGTATCAGACAAAGATCCAGGA 1568  
 |||||||  
 Db 1566 ccagcgcaagatgtactctccagacccatgtacagagccgattacacagaacaagctccagga 1625  
 QY 1569 GAAGTTGCCACTATCATCGGCTCTCGGCGCGCTGGCTGTGTTCTTCTCATTTGCTGTGT 1628  
 |||||||  
 Db 1626 gaagttgcacatcatcatcgtctccctcgccgtgtgcctgtctctcatctgtgtgt 1685  
 QY 1629 TGTTCATCGCATGCTGTGTAAACAGAGGGGGGTTTGAAGCTGCTGACTCGGAGTACACGGA 1688  
 |||||||  
 Db 1686 tgtcatcgcgcatactgtgttaacagagcggggtgttgagcgtgtcactcgtgagttacacgga 1745  
 QY 1689 CAAGTGCACAACATCACCAGTGGCCACATTAACCCAGCATGATGATCATCTCATCTC 1748  
 |||||||  
 Db 1746 caagctgcaaacatacacaagtggtccaatgtacatgtaccccaagtcagtgaatctacatctcc 1805  
 QY 1749 TTTTACCTTACGAGAGACCCCAACGAGGACGTGCGGAGTTGCCAAGAAATTGACATCTC 1808  
 |||||||  
 Db 1806 ttccactctagtgagcaccacagagcagtgcggtgtgttgcgaaggaattgtacatctcc 1865  
 QY 1809 CCGTGTCAAAATTTGACAGAGTATCGGACAGGAGGTTTGGGAGGCTGTGCAAGTGGCCA 1868  
 |||||||  
 Db 1866 cgtgtgcaaaatgtgacaggtgatcggagcaggggtgttgaggtgtgtgtgtgtgtgtgtgt 1925  
 QY 1869 CCTGAAGCTCCAGGACAGAGAGATCTTTGTGGCCATCAAGACCTCAAGTCGGGCTA 1928  
 |||||||  
 Db 1926 cctgaagctcgcaggaagagagatcttltgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1985  
 QY 1929 CACGGAGAAAGCAGCGCGGAGCTTCTGAGCAAGCCTTCATCATGAGGCGAGTTGCACCA 1988  
 |||||||  
 Db 1986 cagggaggaagcagcgccgagatctctgtgagcagcctcatcaltgtgtgtgtgtgtgtgt 2045  
 QY 1989 TCCCAAGCTCATCAACCTGTGAGGAGGTGCTGTGACCAAGACAACTGTGTATATCATCAC 2048  
 |||||||  
 Db 2046 tcccaagctcatcaccacccgt 2105  
 QY 2049 CGAGTTTCATGGAATGGCTCCTGACTCTTTCTCCGGCAAAAGATGGGCGAGTTTAC 2108  
 |||||||  
 Db 2106 cgagttcatgtgagatgtgtcctgt 2165

QY 2109 AGTATCATCAGCTGTGGGACGATGCTTGGGGGACATGAGAGCTGGCATATGATCTGGCAGA 2168  
 |||||||  
 Db 2166 agtcatccagctgt 2225  
 QY 2169 CATGAATATGTTTACCGGTACCTGGCTGGCCGCAACATCTCTGTCAACAGCAACTGGT 2228  
 |||||||  
 Db 2226 catgaatattgtttacacgtgtacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2285  
 QY 2229 CTGCAAGGTGTGGAGCTTGTGGGCTTCACGCTTTTGAAGAGAGATACCTCAACCCAC 2288  
 |||||||  
 Db 2286 ctgcaaggt 2345  
 QY 2289 CTACACAGTGTCCCTGGCGGAAAGTTCCCATCCGCTGTGACAGCCCGAAGCCATCCA 2348  
 |||||||  
 Db 2346 ctacacaggt 2405  
 QY 2349 GTACCGGAAGTTTACCTGGCCAGTATGTGTGTGAGCTTACGGCATTTGTATGTGGAGGT 2408  
 |||||||  
 Db 2406 gtaccggaagttacactcgt 2465  
 QY 2409 GATGTCTTATGGGAGCGGCGCTTACGAGGACATGACCAACAGAGATGTATCAATGTCAT 2468  
 |||||||  
 Db 2466 gatgtcttattggt 2525  
 QY 2469 TGAAGAGACTATCGGCTGTGACCGCCCATGTGAGTGTGCGAGGCGCTTCACCAACTCAT 2528  
 |||||||  
 Db 2526 tgaagagactatcgt 2585  
 QY 2529 GCTGAGCTGTGGCAAGAGACCGCAACACCGGCCCAAGTTGCGCCAAATTGTCAACAC 2588  
 |||||||  
 Db 2586 gctgagctgt 2645  
 QY 2589 GCTAGCAAGATGATCGGATCCGAATCCCAAGCCCTCAAGGCGATGGCGCCCTGCTGCTGG 2648  
 |||||||  
 Db 2646 gctagcaagatgatctgt 2705  
 QY 2649 CATCAACTGTGCGGCTGCTGTGAGCGCACGATGCCCGACTACACAGCTTTTACACGGTGA 2708  
 |||||||  
 Db 2706 catcaactgt 2765  
 QY 2709 CGAGTGTGTGAGGCGCATTAAGATGGGGCAGTACAAAGAGAGCTTTCGCAATGCCGCTT 2768  
 |||||||  
 Db 2766 cgagt 2825  
 QY 2769 CACCTCTTGAAGTGTGTGTGTGATGTGATGTGAGGACATTTCCCGGTTGGGGTCA 2828  
 |||||||  
 Db 2826 cacctcttltgagctgt 2885  
 QY 2829 TTTGGCTGCGCACAGAAAAAATCCTGAACAGTATCCAGGTATGCGGGCGCAGATGA 2888  
 |||||||  
 Db 2886 ttgt 2945  
 QY 2889 CCAGATTACGT 2948  
 |||||||  
 Db 2946 ccagattcagctgt 3005  
 QY 2949 CCGGCCCTCTGC 2962  
 |||||||  
 Db 3006 cccgcccctctgtc 3019

## RESULT 5

AA096250  
ID AA096250 standard; cDNA to mRNA; 171 BP.

AA096250;

22-FEB-1996 (first entry)

Partial DNA encoding human receptor type kinase.

receptor type kinase; osteoblast; screening; anti-cancer; diagnosis;

treatment; bone disease; ds.

KW



```
XX OS Homo sapiens.
XX XX JF07155187-A.
XX PN 20-JUN-1995.
XX PD 03-DEC-1993; 93JP-0303622.
XX PF 03-DEC-1993; 93JP-0303622.
XX PR 03-DEC-1993; 93JP-0303622.
XX PA (ASAH ) ASAH KASEI KOGYO KK.
XX PA WPI: 1995-250736/73.
XX DR P-PSDB; AAR79141.
XX XX Human receptor type tyrosine kinase partial cDNA - used to develop
PT PT medications for the treatment of bone disease caused by
PT proliferation of osteoblast cells
XX PS Claim 1; Page 5; 5pp; Japanese.
XX CC The DNA encodes a human receptor type tyrosine kinase isolated from a
CC human osteoblastoid cell line (MG63) by reverse transcriptase-polymerase
CC chain reaction. The gene fragment can be used for the screening of
CC cells for anti-cancer agents, and for treatment of bone diseases due to
CC the proliferation of osteoblasts.
XX SQ Sequence 171 BP; 39 A; 60 C; 41 G; 31 T; 0 other;

Query Match 4.1%; Score 120; DB 16; Length 171;
Best Local Similarity 99.4%; Pred. No. 9.2e-49;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2203 AACATCCTCTGTACACCACTGCTGTGCAAGTGTGCGACTTTGGCTCTCAGCCTT 2262
DB 1 AACATCCTCTGTACACCACTGCTGTGCAAGTGTGCGACTTTGGCTCTCAGCCTT 60
OY 2263 CTAGAGGAGCATACCTCAGACCCACCTACACAGTGCCTGAGGCGAAGTTCCCAATC 2322
DB 61 CTAGAGGAGCATACCTCAGACCCACCTACACAGTGCCTGAGGCGAAGTTCCCAATC 120
OY 2323 CGCTGGACAGCCCCGAGACCATCCAGTACCGGAAGTTCACTCGGCCAGT 2373
DB 121 CGCTGGAGAGCCCCGAGAGCATCCAGTACCGGAAGTTCACTCGGCCAGT 171

RESULT 6
AA060025
ID AA060025 standard; cDNA; 381 BP.
XX AC AA060025;
XX XX 16-MAR-1994 (first entry)
XX DT 16-MAR-1994 (first entry)
XX DE Human brain Expressed Sequence Tag EST02007.
XX KM Gene transcription product; genetic markers; tagging; in vivo;
XX transcription; mapping; locations; chromosomes; chromosomal; ss.
XX OS Homo sapiens.
XX PN WO9316178-A.
XX PD 19-AUG-1993.
XX PF 12-FEB-1994; 94WO-US01294.
XX PR 12-FEB-1994; 94US-0837195.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX XX
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PI Adams MD, Moreno RF, Venter CJ;
XX DR WPI: 1993-272882/34.
XX XX Enriched oligonucleotides and corresp. sequences - used as
PT PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes
XX PS Example 4; Page 269; 500pp; English.
XX CC The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prepn. of antisense sequences, probes and constructs.
CC EST02007 has been putatively identified as encoding a kinase 5
CC protein. See also AA055041-061440.
XX SQ Sequence 381 BP; 91 A; 100 C; 110 G; 75 T; 5 other;

Query Match 2.9%; Score 85; DB 14; Length 381;
Best Local Similarity 98.9%; Pred. No. 1.3e-31;
Matches 185; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1778 TCGCGAGTTGCCAAGAAATTGACATCTCTGTCAAAATTGACGAGTATCGGAG 1837
DB 35 TCGCGAGTTGCCAAGAAATTGACATCTCTGTCAAAATTGACGAGTATCGGAG 94
OY 1838 CAGGCGAGTTGGCGAGCTGTGCACTGGCCACCTTAAGCTCCAGGCAAGAGAGATCT 1897
DB 95 CAGGCGAGTTGGCGAGCTGTGCACTGGCCACCTTAAGCTCCAGGCAAGAGAGATCT 154
OY 1899 TTGTGGCATCAAGAGCGCTCAAGTGGGCTACACGAGAGAGCGCCGACTTCCTGA 1957
DB 155 TTGTGGCATCAAGAGCGCTCAAGTGGGCTACACGAGAGAGCGCCGACTTCCTGA 214
OY 1958 GCGAAGC 1964
DB 215 GCGAAGC 221

RESULT 7
AA070308
ID AA070308 standard; cDNA; 3105 BP.
XX AC AA070308;
XX XX 19-MAR-1996 (first entry)
XX DT 19-MAR-1996 (first entry)
XX DE Receptor tyrosine kinase (neural kinase) cDNA.
XX KM Receptor tyrosine kinase; neural kinase; Nuk gene; axon;
XX axonogenesis; nerve disorder; gene therapy; transgenic animal; ss.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT CDS 1..2985
XX FT sig_peptide 1..78
XX FT mat_peptide 79..2982
XX FT /*tag= a
XX FT /*tag= b
XX FT /*tag= c
XX PN WO9530326-A1.
XX PD 09-NOV-1995.
XX PR 28-APR-1995; 95WO-CA00254.
XX PF 28-APR-1995; 95WO-CA00254.
XX XX
```

PR 29-APR-1994; 94US-0235407.  
 XX  
 PA (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 XX  
 PI Henkemeyer M, Letwin K, Pawsow A;  
 XX  
 DR WPI; 1995-393299/50.  
 DR P-PSDB; AAR87018.  
 XX  
 PT DNA encoding neural receptor tyrosine kinase - useful in gene  
 PT therapy of nerve disorders, and for diagnosis and identification of  
 PT therapeutic agents  
 XX  
 PS Claim 2; Page 68-70; 103pp; English.  
 XX  
 CC cDNA clones pNURACE A2 and K2 were combined to obtain a sequence  
 CC (AA070308) coding for a novel receptor tyrosine kinase, designated  
 CC neural kinase (Nuk) (AAR87018). The clones were obtd. from a cDNA  
 CC library of mouse embryo cDNA in lambda-gt10 probed with a partial Nuk  
 CC cDNA insert. The gene was mapped to the distal end of chromosome 4  
 CC near the abd-1 mutation. The cDNA is used to produce recombinant  
 CC Nuk or transgenic animal models for studies of Nuk function, or as  
 CC probes to detect genes or diagnose conditions associated with Nuk  
 CC gene mutation, or in gene (antisense) therapy of disorders of the  
 CC nervous system.  
 XX  
 SQ Sequence 3105 BP; 711 A; 937 C; 847 G; 610 T; 0 other;  
 SO  
 Query Match 1.6%; Score 48; DB 16; Length 3105;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1440 GGGCGCTCAAGCCGCGCATCTATGCTTCCAGGTCGGGCGACGCGAC 1487  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1512 gggccctcaagccgcgccatctatgtctccaggtcgggcgacgcac 1559  
 XX  
 RESULT 8  
 AAT84528  
 ID AAT84528 standard; cDNA; 3105 BP.  
 XX  
 AC AAT84528;  
 XX  
 DT 02-DEC-1997 (first entry)  
 DE  
 XX Mouse Nuk tyrosine kinase cDNA.  
 DE  
 XX Nuk tyrosine kinase; Eph receptor tyrosine kinase;  
 KW signal transduction; axonogenesis; neurodegenerative disease;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW multiple sclerosis; amyotrophic lateral sclerosis;  
 KW Wernicke's disease; nerve damage; trauma; ischaemia; stroke; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2985  
 FT sig\_peptide 1..78  
 FT mat\_peptide 79..2982  
 FT /\*tag= b  
 FT /\*tag= c  
 XX  
 PN WO9714966-A1.  
 PD 24-APR-1997.  
 XX  
 PF 10-OCT-1996; 96WO-CA00679.  
 XX  
 PR 13-OCT-1995; 95US-0005518.  
 XX  
 PA (MOUN ) MOUNT SINAI HOSPITAL CORP.

XX  
 PI Henkemeyer M, Pawsow A;  
 XX  
 DR WPI; 1997-245245/22.  
 DR P-PSDB; AAW26366.  
 XX  
 PT Activation of ligand regulatory pathways by Eph subfamily receptor  
 PT tyrosine kinases - for stimulating or inhibiting axonogenesis,  
 PT useful for treatment of e.g. neurodegenerative diseases such as  
 PT Alzheimer's or Parkinson's diseases  
 XX  
 PS Disclosure; Page 24-25; 55pp; English.  
 XX  
 CC This cDNA sequence codes for murine Nuk tyrosine kinase (AAW26366),  
 CC an Eph subfamily receptor tyrosine kinase essential for formation  
 CC of the medial tract of the anterior commissure of the brain. Its  
 CC sequence was deduced from clones isolated from an embryo cDNA  
 CC library in lambda gt10. The Nuk gene maps to the distal end of  
 CC chromosome 4 near the abd-1 mutation. Eph subfamily receptor  
 CC tyrosine kinases (e.g. Nuk extracellular domain polypeptides)  
 CC can be used in claimed methods to: activate a ligand regulatory  
 CC pathway in a cell; identify a substance able to bind a ligand for  
 CC an Eph subfamily receptor tyrosine kinase; and to affect neuronal  
 CC development or regeneration, especially the stimulation or  
 CC inhibition of axonogenesis, in a mammal. Activation of the ligand  
 CC regulatory pathway results in downstream activation of a series of  
 CC regulatory pathways in cells that control gene expression, cell  
 CC division, cytoskeletal architecture, cell metabolism, cell  
 CC migration and cell-cell interactions. Substances which activate  
 CC the ligand regulatory pathway may be used for stimulating or  
 CC inhibiting neuronal development, regeneration and axonal migration  
 CC associated with neurodegenerative disease e.g. Alzheimer's,  
 CC Parkinson's or Huntington's diseases, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, deficiency diseases such as  
 CC Wernicke's disease, peripheral nerve damage, trauma and ischaemia  
 CC resulting from stroke.  
 XX  
 SQ Sequence 3105 BP; 710 A; 937 C; 848 G; 610 T; 0 other;  
 SO  
 Query Match 1.6%; Score 48; DB 18; Length 3105;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1440 GGGCGCTCAAGCCGCGCATCTATGCTTCCAGGTCGGGCGACGCGAC 1487  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1512 gggccctcaagccgcgccatctatgtctccaggtcgggcgacgcac 1559  
 XX  
 RESULT 9  
 AAQ90655  
 ID AAQ90655 standard; cDNA; 3776 BP.  
 XX  
 AC AAQ90655;  
 XX  
 DT 11-NOV-1995 (first entry)  
 DE  
 XX Eph-related PTK Cdk5 cDNA.  
 DE  
 XX Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
 KW prognosis; ss.  
 XX  
 OS Gallus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 290..3311  
 FT /\*tag= a  
 XX  
 PN WO9515375-A.  
 PD 08-JUN-1995.  
 XX  
 PF 07-SEP-1994; 94WO-US10140.  
 XX

XX 03-DEC-1993; 93US-0162809.  
XX (LJOL-) LA JOLLA CANCER RES FOUND.  
XX  
XX Pasquale EB, Sajjadi FG;  
XX  
XX WPI: 1995-215256/28.  
XX P-PSDB: AAR75707.  
XX  
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
XX cancer.  
XX  
XX Claim 2; Page 50-53; 129pp; English.  
XX  
XX Novel Eph-related PTK cDNA clone Cek9 (given in AA090655) was  
XX isolated from a chick embryo library in lambda. Cek9 protein  
XX (AAR75707) is closely related to Csk5 (AAR75712). In adult tissues,  
XX Cek9 expression is predominant in the thymus and detectable in  
XX brain, retina, kidney, lung and heart.  
XX  
XX Sequence 3776 BP; 1005 A; 881 C; 941 G; 949 T; 0 other;

Query Match 1.1%; Score 32; DB 16; Length 3776;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2389 GGCATGTCATGCGAGCTGATGCTCATG 2420  
DB 2687 ggcattgcatcgtggaagtgatgctcatg 2718

RESULT 10  
AA062461  
ID AA062461 standard; cDNA: 3751 BP.  
XX  
XX AA062461:  
XX  
XX 09-NOV-1994 (first entry)  
XX  
XX Human embryonal kinase 2 receptor.  
XX  
XX Embryonal kinase; HEK; protein tyrosine kinase; PTK; tumour;  
XX cancer; therapy; amplification; primer; polymerase chain reaction;  
XX PCR; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 1..2973  
XX FT /\*tag= a  
XX  
XX DE4233782-A.  
XX  
XX 14-APR-1994.  
XX  
XX 07-OCT-1992; 92DE-4233782.  
XX  
XX 07-OCT-1992; 92DE-4233782.  
XX  
XX 07-OCT-1992; 92DE-4233782.  
XX  
XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.  
XX  
XX Holtrich U, Ruebsamen-Walpmann H, Strebhardt K;  
XX  
XX WPI: 1994-127194/16.  
XX P-PSDB: AAR51899.  
XX  
XX Human embryonal kinase 2-receptor protein - useful in tumour  
XX diagnosis and therapy  
XX  
XX Claim 4; Page 7-10; 11pp; German.  
XX

CC RNA from human embryonic tissue was isolated. With the use of  
CC primer P6(4) PTK-specific cDNA was synthesised. The cDNA was  
CC amplified using primers P6(4) and N5. A 2097 bp DNA fragment was  
CC obtained. Primers E3, P12 and E6 were then used in the isolation of  
CC the C-terminal of the HEK2 receptor gene.  
XX  
XX Sequence 3751 BP; 739 A; 1150 C; 1123 G; 739 T; 0 other;

Query Match 1.0%; Score 30; DB 15; Length 3751;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 GGGTGGGAAGAGGTGAGTGCCTACGATGAG 111  
DB 157 ggcgtggaagaggtgagtgctacgatacg 186

RESULT 11  
AA090652  
ID AA090652 standard; cDNA: 3133 BP.  
XX  
XX AA090652:  
XX  
XX 11-NOV-1995 (first entry)  
XX  
XX Eph-related tyrosine kinase CEK6 cDNA.  
XX  
XX Cek6; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
XX prognosis; ss.  
XX  
XX Gallus sp.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 3..419  
XX FT /\*tag= a  
XX CDS 421..2859  
XX FT /\*tag= b

XX  
XX W09515375-A.  
XX  
XX 08-JUN-1995.  
XX  
XX 07-SEP-1994; 94WO-US10140.  
XX  
XX 03-DEC-1993; 93US-0162809.  
XX  
XX (LJOL-) LA JOLLA CANCER RES FOUND.  
XX  
XX  
XX Pasquale EB, Sajjadi FG;  
XX  
XX WPI: 1995-215256/28.  
XX P-PSDB: AAR75704.  
XX  
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
XX cancer.  
XX  
XX Disclosure: Page 37-41; 129pp; English.  
XX  
XX  
XX Novel Eph-related PTK Cek6 cDNA clones (AA090652) were isolated from  
XX chick embryo and embryonic brain cDNA libraries in phage lambda gtl1.  
XX The encoded Cek6 protein (AAR75704) is closely related to rat Elk,  
XX Csk5 (AAR75712) and Csk10 (AAR75708). Cek6 transcripts were found in  
XX 10-day embryos and in adult brain, lung, heart and skeletal muscle.  
XX  
XX Sequence 3133 BP; 718 A; 918 C; 922 G; 575 T; 0 other;

Query Match 1.0%; Score 29; DB 16; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 271 GGCTCTGCAAGAGACCTTCAACCTCTA 299

Db 255 ggcctcgcgaagagacctcaacctcta 283  
|||||

## RESULT 12

AAV70208  
ID AAV70208 standard; DNA; 3592 BP.

AAV70208;

DT 11-FEB-1999 (first entry)

DE Rat receptor tyrosine kinase Etk-2 encoding DNA.

KM Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;

KW neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;

OS binding protein; BDNF; NR-3; diagnosis; ss.

XX Rattus sp.

XX Key Location/Qualifiers

FT CDS 598..3444

FT /\*tag= a

PF 06-JUN-1995; 95US-0469537.

PR 17-MAR-1995; 95US-0406247.

PR 26-JUL-1991; 91US-0736559.

PR 28-OCT-1993; 93US-0144992.

PR 06-JUN-1995; 95US-0469537.

XX (REGF-) REGENERON PHARM INC.

XX Maisompierre PC, Maslakowski P, Yancopoulos GD;

XX WPI; 1999-044584/04.

XX P-PSDB; AAW83148.

XX DNA encoding receptor tyrosine kinase proteins - and corresponding

XX proteins

XX Claim 7; Fig 21; 194pp; English.

XX The present invention describes nucleic acid molecules for ror-1,

XX ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:

XX Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor

XX tyrosine kinases. The present sequence encodes rat Etk-2.

XX Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T; 2 other;

XX Query Match 1.0%; Score 29; DB 20; Length 3592;

XX Best Local Similarity 100.0%; Pred. No. 0.00035;

XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2392 ATGTGATGAGGAGGATGCTGCTATGG 2420

Db 3184 atgtcatgtggaagtgatgtctatgg 3212

RESULT 13

AAQ90660

ID AAQ90660 standard; DNA; 4049 BP.

XX AAQ90660;

AC AAQ90660;

XX 11-NOV-1995 (first entry)

XX Eph-related PTK Cdk5.

XX Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

KW prognosis; ss.

XX Gallus sp.

OS Gallus sp.

XX Key Location/Qualifiers

FT CDS 10..2997

FT /\*tag= a

PN W09515375-A.

PD 08-JUN-1995.

XX 07-SEP-1994; 94MO-US10140.

PF 03-DEC-1993; 93US-0162809.

PR (LJOL-) LA JOLLA CANCER RES FOUND.

XX Pasquale EB, Sajjadi FG;

XX WPI; 1995-215256/28.

XX P-PSDB; AAR75712.

XX Etk-related protein tyrosine kinase(s) - for monitoring and diagnosing

XX cancer.

XX Disclosure; Page 92-96; 129pp; English.

XX Probes derived from the Eph-related PTKs Cdk4 (AAQ90659) and Cdk5

XX (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58,

XX AAQ90661-62) from chicken embryo and embryonic brain libraries.

XX Sequence 4049 BP; 1010 A; 1011 C; 1072 G; 956 T; 0 other;

XX Query Match 1.0%; Score 29; DB 16; Length 4049;

XX Best Local Similarity 100.0%; Pred. No. 0.00035;

XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 GTCAACGACACCTGCTGCAAGGTGTC 2240

Db 2296 gtcaacagcaacctgtctgcaaggtgtc 2324

RESULT 14

AAQ90657

ID AAQ90657 standard; DNA; 4097 BP.

XX AAQ90657;

XX 11-NOV-1995 (first entry)

XX Eph-related PTK Cdk5+.

XX Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

XX prognosis; ss.

XX Gallus sp.

XX Key Location/Qualifiers

FT CDS 10..3045

FT /\*tag= a

PN W09515375-A.

PD 08-JUN-1995.

XX 07-SEP-1994; 94MO-US10140.

XX 03-DEC-1993; 93US-0162809.

PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Pasquale EB, Sajjadi FG;  
 XX  
 DR WPI: 1995-215256/28.  
 XX  
 DR P-PSDB: AAR75709.  
 XX  
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 PT cancer.  
 PS  
 PS Claim 2; Page 71-75; 129pp: English.  
 XX  
 CC A cDNA clone encoding a novel variant of EPH-related PTK Cdk5,  
 CC Cdk5+ (AA090657), was isolated from a chick embryo library in  
 CC lambda gtl1. Cdk5+ protein (AAR75709) contains a 16-amino acid  
 CC insertion in the juxtamembrane domain, and be a result of  
 CC alternative splicing. Cdk5+ is exclusively expressed in the CNS.  
 CC  
 SQ Sequence 4097 BP; 1014 A; 1029 C; 1087 G; 967 T; 0 other;

Query Match 1.0%; Score 29; DB 16; Length 4097;  
 Best Local Similarity 100.0%; Pred. No. 0.00035;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2212 GTCACAGCAGCAGCTGCTGTCGACAGGTGC 2240  
 ||||||||||||||||||||||||||||  
 DB 2344 gtcaacagcaacctgctgtcgaagtgtc 2372

## RESULT 15

AA053470  
 ID AA053470 standard; DNA: 1509 BP.

AC AA053470;

DT 16-JUN-1994 (first entry)

DE PTK gene B1.

XX  
 KW Lambda gtl1; expression vector: lambda-B1-Elk; protein tyrosine kinase:  
 KW Elk; B1; Eph; subfamily; receptor-like tyrosine kinase; eph; eck;  
 KW phosphorylation; phosphorylated kinase insert domain; growth factor;  
 KW receptor kinase; platelet-derived growth factor receptor; ss.

OS Rattus rattus.

XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1143  
 FT /\*tag= a  
 FT /product= Elk

PN CA2083521-A.

PD 01-OCT-1993.

PF 23-NOV-1992; 92CA-2083521.

PR 31-MAR-1992; 92US-0861390.

PA (MOUN ) MOUNT SINAI HOSPITAL CORP.

PI Letwin K, Pawson A, Reedijk M;

DR WPI: 1993-406300/51.

DR P-PSDB: AAR44512.

XX  
 PT Expression of phosphorylated exogenous protein - in host cells  
 PT transformed with two vectors, one for the protein, the other for  
 PT catalytic domain of protein kinase

PS Disclosure: Fig 1; 55pp: English.  
 XX

CC This sequence represents a fragment of the lambda gtl1 expression  
 CC vector, lambda-B1-Elk, which encodes the catalytic sequence of the  
 CC protein tyrosine kinase, Elk. The Elk gene, B1, encodes a protein  
 CC which is a member of the Eph subfamily of protein tyrosine kinases.  
 CC The Elk product is very similar to two other receptor-like tyrosine  
 CC kinases, eph and eck. Lambda-B1-Elk may be used in the production  
 CC of phosphorylated exogenous protein along with a further vector  
 CC encoding the desired exogenous protein. These plasmid may be used  
 CC to produce phosphorylated proteins in host cells which have no  
 CC intrinsic capacity for phosphorylation, eg. bacteria. The system  
 CC may be used for the expression of the phosphorylated kinase insert  
 CC domain of a growth factor receptor kinase eg. platelet-derived growth  
 CC factor receptor.  
 CC  
 SQ Sequence 1509 BP; 393 A; 374 C; 429 G; 313 T; 0 other;

Query Match 0.9%; Score 26; DB 14; Length 1509;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2524 CTCATGCTGACACTGTGACAGAGA 2549  
 ||||||||||||||||||||||||  
 DB 754 ctcatgctgacctgttgacagaaga 779

Search completed: July 10, 2001, 21:22:37  
 Job time: 9649 sec







Db 61 TGGATGGATCCCTCCATCAGGGGTGGGAAGAGGTGATGGCTACGATGAGAAATGATGAC 120  
Qy 121 AGGATCCGACAGTACAGAGGTGCAAGCTGTTAGTCAAGCCGAACAACTGGCTACGG 180  
Db 121 AGGATCCGACAGTACAGAGGTGCAAGCTGTTAGTCAAGCCGAACAACTGGCTACGG 180  
Qy 181 ACCAAGTTTATCCGGCCCGGTGGGGCCACCGCATCCACGTGGAGATGAAGTTTTCGGTG 240  
Db 181 ACCAAGTTTATCCGGCCCGGTGGGGCCACCGCATCCACGTGGAGATGAAGTTTTCGGTG 240  
Qy 241 CGTACTGCAAGCAGATCCCGAGGCTGTGGCTCTGCAAGAGAGACTTCAACCTCTAT 300  
Db 241 CGTACTGCAAGCAGATCCCGAGGCTGTGGCTCTGCAAGAGAGACTTCAACCTCTAT 300  
Qy 301 TACTATGAGGCTGACTTGTGATGCTGGCCACCAAGACCTTCCCAACTGGATGGAAATCCA 360  
Db 301 TACTATGAGGCTGACTTGTGATGCTGGCCACCAAGACCTTCCCAACTGGATGGAAATCCA 360  
Qy 361 TGGGTGAAGGTGATATACATTTGACAGCCGAGAGACTTTCGCCAGTGGAGCTGGGTGGC 420  
Db 361 TGGGTGAAGGTGATATACATTTGACAGCCGAGAGACTTTCGCCAGTGGAGCTGGGTGGC 420  
Qy 421 CGGCTCATGAAAATCAACACCGAGGTGCGAGCTTGGAGCTGTGTCGCCAGCGGCTTC 480  
Db 421 CGGCTCATGAAAATCAACACCGAGGTGCGAGCTTGGAGCTGTGTCGCCAGCGGCTTC 480  
Qy 481 TACTGGCCCTCCAGAGCTATGGCGGTGATGTCCCTCATCCGCGGTGCTTCTAC 540  
Db 481 TACTGGCCCTCCAGAGCTATGGCGGTGATGTCCCTCATCCGCGGTGCTTCTAC 540  
Qy 541 CGCAAGTGGCCCGCATCATCCAGAAATGGCGCATCTTCAGAGAAACCTGTGGGGGCT 600  
Db 541 CGCAAGTGGCCCGCATCATCCAGAAATGGCGCATCTTCAGAGAAACCTGTGGGGGCT 600  
Qy 601 GAAGAGCATGCTGCTGGTGGCTGCCCGGGGAGCTGCATGCCAATGCGAAGAGGTGAT 660  
Db 601 GAAGAGCATGCTGCTGGTGGCTGCCCGGGGAGCTGCATGCCAATGCGAAGAGGTGAT 660  
Qy 661 GTACCCATCAAGCTCTACTGTAAAGGGGAGGGAGGTGGTGGCCCATCGGGGCTGC 720  
Db 661 GTACCCATCAAGCTCTACTGTAAAGGGGAGGGAGGTGGTGGCCCATCGGGGCTGC 720  
Qy 721 ATGTGCAAAAGCAGGCTTGCAGGCGTGTGAAATGAGCAGCTGTGCCAGAGTTTCCATCT 780  
Db 721 ATGTGCAAAAGCAGGCTTGCAGGCGTGTGAAATGAGCAGCTGTGCCAGAGTTTCCATCT 780  
Qy 781 GGGACTTTCAAGGCCAACCAGGGGATGAGGCTGTACCCACTGTCCCATCAACACCGG 840  
Db 781 GGGACTTTCAAGGCCAACCAGGGGATGAGGCTGTACCCACTGTCCCATCAACACCGG 840  
Qy 841 ACCACTTTGAAAGGGGACCAACACTGTGTGCGCAATGGCTACTACAGAGAGACTG 900  
Db 841 ACCACTTTGAAAGGGGACCAACACTGTGTGCGCAATGGCTACTACAGAGAGACTG 900  
Qy 901 GACCCCTTGACATGCGCTGCAACACCATCCCTCGCGCCCGAGGCTGTGATTTCCAGT 960  
Db 901 GACCCCTTGACATGCGCTGCAACACCATCCCTCGCGCCCGAGGCTGTGATTTCCAGT 960  
Qy 961 GTCAATGAGACCTCCCTCAATGCTGGAGTGGAGCCCTCCCGCGAGCTCGGAGGCGAGAG 1020  
Db 961 GTCAATGAGACCTCCCTCAATGCTGGAGTGGAGCCCTCCCGCGAGCTCGGAGGCGAGAG 1020  
Qy 1021 GACCTGCTTACACATCATCTGTGCAAGAGACTGTGGTGGGGCGGGGTCTGTGCAACCGC 1080  
Db 1021 GACCTGCTTACACATCATCTGTGCAAGAGACTGTGGTGGGGCGGGGTCTGTGCAACCGC 1080  
Qy 1081 TCCGGGAGCAATGATAGTACGACCGCAGCTAGAGGCTGACGAGGCAAGCATTTAC 1140  
Db 1081 TCCGGGAGCAATGATAGTACGACCGCAGCTAGAGGCTGACGAGGCAAGCATTTAC 1140  
Qy 1141 ATCAGTGAACCTGTGGCCACAGCCAGTACACTTCGAAATCCAGGCTGTGAAGGCGTT 1200  
Db 1141 ATCAGTGAACCTGTGGCCACAGCCAGTACACTTCGAAATCCAGGCTGTGAAGGCGTT 1200

Db 1141 ATCAGTGAACCTGTGGCCACAGCCAGTACACTTCGAAATCCAGGCTGTGAAGGCGTT 1200  
Qy 1201 ACTGACCAAGCCCTTCTGCGCTCAAGTTGCTGTGAAATCACCACCAACAGGCA 1260  
Db 1201 ACTGACCAAGCCCTTCTGCGCTCAAGTTGCTGTGAAATCACCACCAACAGGCA 1260  
Qy 1261 GCTTCATGCGCAGTGTCCATCATGATCAGTGAAGCGGCAACCGTGGACATTTACCTG 1320  
Db 1261 GCTTCATGCGCAGTGTCCATCATGATCAGTGAAGCGGCAACCGTGGACATTTACCTG 1320  
Qy 1321 TCGTGTCCAGCCGAGACAGCCCAATGGCGTATCCGTGACTATGAGCTGACACTAT 1380  
Db 1321 TCGTGTCCAGCCGAGACAGCCCAATGGCGTATCCGTGACTATGAGCTGACACTAT 1380  
Qy 1381 GAGAGAGCTCAGTGAATCAAGCCACAGCCATAAAGCCCAACACAGGTCAG 1440  
Db 1381 GAGAGAGCTCAGTGAATCAAGCCACAGCCATAAAGCCCAACACAGGTCAG 1440  
Qy 1441 GGCTCAAGCCGGCGCATATGCTTCCAGTGGCGGACAGCATGTGGAGGCTAC 1500  
Db 1441 GGCTCAAGCCGGCGCATATGCTTCCAGTGGCGGACAGCATGTGGAGGCTAC 1500  
Qy 1501 GGGCGCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAACCGAGTACAGACAAC 1560  
Db 1501 GGGCGCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAACCGAGTACAGACAAC 1560  
Qy 1561 ATCCAGAGCAATTTGCATCATATGCGCTCTGGCGGCTGGCTGTGCTCTCAT 1620  
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Qy 1621 GCTGTGTTGTCATGCGCATGCTGTGTAAACAGAGGGGGTTGAGGCTGTGCTGTGAG 1680  
Db 1621 GCTGTGTTGTCATGCGCATGCTGTGTAAACAGAGGGGGTTGAGGCTGTGCTGTGAG 1680  
Qy 1681 TACACGAGCAAGTTCACACTACACAGTGGCCACATTAACCCACAGCATGAAGATCAC 1740  
Db 1681 TACACGAGCAAGTTCACACTACACAGTGGCCACATTAACCCACAGCATGAAGATCAC 1740  
Qy 1741 ATCGATCTTTTCACTTACAGAGACCCCAACAGGCAAGTCCGGAGTTTCCCAAGAAAT 1800  
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Qy 1801 GACATCTCTGTTCAAAATTTGAGCAGGTGATGCGAGGAGGAGTTTGGGAGGCTGTC 1860  
Db 1801 GACATCTCTGTTCAAAATTTGAGCAGGTGATGCGAGGAGGAGTTTGGGAGGCTGTC 1860  
Qy 1861 AGTGGCCACCTGAAGCTGCCAGGCAAGAGAGATCTTGTGGCCATCAAGACGCTCAAG 1920  
Db 1861 AGTGGCCACCTGAAGCTGCCAGGCAAGAGAGATCTTGTGGCCATCAAGACGCTCAAG 1920  
Qy 1921 TCGGGCTTACAGGAGCAAGAGGCGCGGACTCTGAGGGAAGCCCTCATTCATGGGCCAG 1980  
Db 1921 TCGGGCTTACAGGAGCAAGAGGCGCGGACTCTGAGGGAAGCCCTCATTCATGGGCCAG 1980  
Qy 1981 TTGACCATCCCAACGTCTCCACTGAGGAGGTGTGTCGACCAAGAGCACACTGTGATG 2040  
Db 1981 TTGACCATCCCAACGTCTCCACTGAGGAGGTGTGTCGACCAAGAGCACACTGTGATG 2040  
Qy 2041 ATCATCACCAGTTCATGAGAGATGGCTCCGTGACCTCTTCTCCGGCAAAACGATGGG 2100  
Db 2041 ATCATCACCAGTTCATGAGAGATGGCTCCGTGACCTCTTCTCCGGCAAAACGATGGG 2100  
Qy 2101 CAGTTACAGTATCATCAGTGTGGATGCTTCCGGGGCATGCGAGCGCATGGAATGAC 2160  
Db 2101 CAGTTACAGTATCATCAGTGTGGATGCTTCCGGGGCATGCGAGCGCATGGAATGAC 2160  
Qy 2161 CTGGAGACATGAATATGTTACCCGTGACCTGTCGCCGCAACATCTGTCAACAGC 2220  
Db 2161 CTGGAGACATGAATATGTTACCCGTGACCTGTCGCCGCAACATCTGTCAACAGC 2220  
Qy 2221 AACCTGCTGTGAAGGTGCGACTTTGGGCTCTACGCTTTCTAGAGAGCATACCTCA 2280  
Db 2221 AACCTGCTGTGAAGGTGCGACTTTGGGCTCTACGCTTTCTAGAGAGCATACCTCA 2280

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Oy 2281 GACCCACCTACACAGTGGCTGGGCGGAAAGTTCCCATCCGCTGGACAGCCCGGAA 2340
    |||||||
Db 2281 GACCCACCTACACAGTGGCTGGGCGGAAAGTTCCCATCCGCTGGACAGCCCGGAA 2340
Oy 2341 GCCATCAGTACCGGAAATGACCTCGGCGCATGTGTGTGAGCTACGGCATTTCTCATG 2400
    |||||||
Db 2341 GCCATCAGTACCGGAAATGACCTCGGCGCATGTGTGTGAGCTACGGCATTTCTCATG 2400
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Db 2401 TGGGAGTGATGTCTTATGGGAGGCGGCGTACGTGGACATGACCAACAGAGATTAATC 2460
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    |||||||
Db 2461 AATGCAATTTGAGCAGAGATATGCGCTGCCACCGCCCATGAGACTGGCCGAGCCCTGCAC 2520
Oy 2521 CAATCTATGCTGAGCTGTTGGCAGAGACCGCAACACCGGCCCAAGTTGGCCCAATT 2580
    |||||||
Db 2521 CAATCTATGCTGAGCTGTTGGCAGAGACCGCAACACCGGCCCAAGTTGGCCCAATT 2580
Oy 2581 GTCAACACGCTAGACAGATGATCCGCAATCCCAACAGCTTAAGGCCATGGCCGCTC 2640
    |||||||
Db 2581 GTCAACACGCTAGACAGATGATCCGCAATCCCAACAGCTTAAGGCCATGGCCGCTC 2640
Oy 2641 TCCTCTGCGATCAACCTGCGCTGCTGACCGACGATCCCGACTACACAGCTTTAAC 2700
    |||||||
Db 2641 TCCTCTGCGATCAACCTGCGCTGCTGACCGACGATCCCGACTACACAGCTTTAAC 2700
Oy 2701 ACGGTGACAGATGCTGTGAGGCGCATCAAGATGGGCGAGTACAGAGAGCTTCCCAAT 2760
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Db 2701 ACGGTGACAGATGCTGTGAGGCGCATCAAGATGGGCGAGTACAGAGAGCTTCCCAAT 2760
Oy 2761 GCCGCGTACCTGCTTGTGACGTCGTCTCAGATGATGAGAGACATTTCTCCGGGTT 2820
    |||||||
Db 2761 GCCGCGTACCTGCTTGTGACGTCGTCTCAGATGATGAGAGACATTTCTCCGGGTT 2820
Oy 2821 GGGGTCACCTTGGCTGGCCACGAGAAAAAATCTGMAACGATGATGAGGCGG 2880
    |||||||
Db 2821 GGGGTCACCTTGGCTGGCCACGAGAAAAAATCTGMAACGATGATGAGGCGG 2880
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Db 2881 CAGATGAACCAATTCAGTCTGTGGAGGTTTGACATTCACCTGCGCTACACCTTTC 2940
Oy 2941 CTCGACGCGCGCGCTCTGC 2962
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Db 2941 CTCGACGCGCGCGCTCTGC 2962

```

## RESULT 2

```

US-08-702-367A-10
Sequence 10, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A

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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2962 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2913
; US-08-702-367A-10

Query Match 100.0%; Score 2962; DB 2; Length 2962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGTCGCGCGCGTGGAGAAACGCTAATGAGCTCACTACAGGAGCTGTGAGCTGGC 60
    |||||||
Db 1 CTGTCGCGCGCGTGGAGAAACGCTAATGAGCTCACTACAGGAGCTGTGAGCTGGC 60
Oy 61 TGGATGTGATCTCTTCATCAGGTGGGAGAGGTGAGTGGCTACATGAGAACATGAAAC 120
    |||||||
Db 61 TGGATGTGATCTCTTCATCAGGTGGGAGAGGTGAGTGGCTACATGAGAACATGAAAC 120
Oy 121 ACGATCCGACGTACCAAGTGTGCAACGTGTTAGTCAAGCCAGAACACAGCTGGCTAGG 180
    |||||||
Db 121 ACGATCCGACGTACCAAGTGTGCAACGTGTTAGTCAAGCCAGAACACAGCTGGCTAGG 180
Oy 181 ACCAAGTTTATCCGCGCGCGTGGGCGCCACCGCATCACTGAGAGATGAAGTTTTCGGTG 240
    |||||||
Db 181 ACCAAGTTTATCCGCGCGCGTGGGCGCCACCGCATCACTGAGAGATGAAGTTTTCGGTG 240
Oy 241 CGTGAACGACGACGATCCCGACGCTGCTGCTCTGCAAGAGAACTTCAACCTTAT 300
    |||||||
Db 241 CGTGAACGACGACGATCCCGACGCTGCTGCTCTGCAAGAGAACTTCAACCTTAT 300
Oy 301 TACTATGAGGCTGATGCTTGTGACTCGGCGACCAAGACCTTCCCACTGATGAGAAATCCA 360
    |||||||
Db 301 TACTATGAGGCTGATGCTTGTGACTCGGCGACCAAGACCTTCCCACTGATGAGAAATCCA 360
Oy 361 TGGGTGAAGTGTGATACATTCGACCGGAGAGAGCTTCTCCAGGTGAGACTGGGTGGC 420
    |||||||
Db 361 TGGGTGAAGTGTGATACATTCGACCGGAGAGAGCTTCTCCAGGTGAGACTGGGTGGC 420
Oy 421 CGCGTCATGAAATCAACACGAGGTGCGGAGCTTCCGACCTGTGTCCGCGACGGGCTTC 480
    |||||||
Db 421 CGCGTCATGAAATCAACACGAGGTGCGGAGCTTCCGACCTGTGTCCGCGACGGGCTTC 480
Oy 481 TACCTGGCTTCAGAGACTATGCGGCTGCAATGCTCATGCTGCTGCTGTCTTCTTAC 540
    |||||||
Db 481 TACCTGGCTTCAGAGACTATGCGGCTGCAATGCTCATGCTGCTGCTGTCTTCTTAC 540
Oy 541 CCGAAGTCCCGCGCATCATCCAGATGCGGCGCATCTTCCAGAAACCTGTGCGGGGCT 600
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Db 541 CCGAAGTCCCGCGCATCATCCAGATGCGGCGCATCTTCCAGAAACCTGTGCGGGGCT 600
Oy 601 GAGAGACATCGCTGTGCTGCTGCGGCGGAGCTGATGCGCAATGCGGAAGAGTGGAT 660
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Db 601 GAGAGACATCGCTGTGCTGCTGCGGCGGAGCTGATGCGCAATGCGGAAGAGTGGAT 660
Oy 661 GTACCCATCAAGCTTACTGTAAAGGAGGCGGAGTGGCTGTGCGGCGCTGC 720
    |||||||
Db 661 GTACCCATCAAGCTTACTGTAAAGGAGGCGGAGTGGCTGTGCGGCGCTGC 720
Oy 721 AATGCAAGACAGCTTTCAGGCGGCTTGAAGATGCAACCGCTGTGCGGAGTGTCCATCT 780
    |||||||
Db 721 AATGCAAGACAGCTTTCAGGCGGCTTGAAGATGCAACCGCTGTGCGGAGTGTCCATCT 780

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QY 781 GGGACCTTCAAGGCCAACCAAGGGGATGAGGCGCTGTACCCACTGTGCCATCAACAGCCGG 840  
|||||  
Db 781 GGGACCTTCAAGGCCAACCAAGGGGATGAGGCGCTGTACCCACTGTGCCATCAACAGCCGG 840  
QY 841 ACCACTTCTGAAGGGGGCCACCACACTGTGTCCGCAATGGCTACTACAGAGAGACCTG 900  
|||||  
Db 841 ACCACTTCTGAAGGGGGCCACCACACTGTGTCCGCAATGGCTACTACAGAGAGACCTG 900  
QY 901 GACCCCTGGACATGCTCCCTGACAAACCATCCCTCCGCGCCCGACGGCTGTATTTCCAGT 960  
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Db 901 GACCCCTGGACATGCTCCCTGACAAACCATCCCTCCGCGCCCGACGGCTGTATTTCCAGT 960  
QY 961 GTCAATGAGACTCCCTCATCTGTGAGTGAACCCCTCCCGCGACTCCGGAGGGCCGAGAG 1020  
|||||  
Db 961 GTCAATGAGACTCCCTCATCTGTGAGTGAACCCCTCCCGCGACTCCGGAGGGCCGAGAG 1020  
QY 1021 GACCTCGTCTCAACATCATCTGTGAAGAGCTGTGGCTCGGGCCGGGGTCCCTGCAACCCG 1080  
|||||  
Db 1021 GACCTCGTCTCAACATCATCTGTGAAGAGCTGTGGCTCGGGCCGGGGTCCCTGCAACCCG 1080  
QY 1081 TGGCGGGACATGTACAGTACGACACGCGGAGCTAGGCGCTGACGAGCCGACGATTTAC 1140  
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Db 1081 TGGCGGGACATGTACAGTACGACACGCGGAGCTAGGCGCTGACGAGCCGACGATTTAC 1140  
QY 1141 ATCAGTGACTGTGGGCCACACCCAGTACACTTTGAGATCCAGGCTGTGAGAGCGGTT 1200  
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Db 1141 ATCAGTGACTGTGGGCCACACCCAGTACACTTTGAGATCCAGGCTGTGAGAGCGGTT 1200  
QY 1201 ACTGACCAAGCCCTTCTGCGCTCACTGTGCGCTGTGAAACATCACACCACCAAGGCA 1260  
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Db 1201 ACTGACCAAGCCCTTCTGCGCTCACTGTGCGCTGTGAAACATCACACCACCAAGGCA 1260  
QY 1261 GCTTCATCGGCAAGTGTCCATCATGATCAGTGTGAGCGGACACCGTGGAGAGATTACCTG 1320  
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Db 1261 GCTTCATCGGCAAGTGTCCATCATGATCAGTGTGAGCGGACACCGTGGAGAGATTACCTG 1320  
QY 1321 TCGTGTGCCAGCGGACACGACCCCAATGGCGTGTCTGTGAACTATGAGCTGACTAT 1380  
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Db 1321 TCGTGTGCCAGCGGACACGACCCCAATGGCGTGTCTGTGAACTATGAGCTGACTAT 1380  
QY 1381 GAGAAAGAGCTGAGTGAATCAAGCGGACAGCCATAAAGCCGCCACACAGCGGTACG 1440  
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Db 1381 GAGAAAGAGCTGAGTGAATCAAGCGGACAGCCATAAAGCCGCCACACAGCGGTACG 1440  
QY 1441 GGCCTCAAGCCGGCGGCACTATGTCTTCCAGGTGGCGGACAGCACTGTGGAGGCTAC 1500  
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Db 1441 GGCCTCAAGCCGGCGGCACTATGTCTTCCAGGTGGCGGACAGCACTGTGGAGGCTAC 1500  
QY 1501 GGGCGCTACAGCGGCAAGATGTACTTCCAGCATGACAGACAGCCGAGTACGACAGAC 1560  
|||||  
Db 1501 GGGCGCTACAGCGGCAAGATGTACTTCCAGCATGACAGACAGCCGAGTACGACAGAC 1560  
QY 1561 ATCCAGGAGAAGTGGCACTATCATGAGGCTCTCGGCGGCTGGCGTGTCTTCAT 1620  
|||||  
Db 1561 ATCCAGGAGAAGTGGCACTATCATGAGGCTCTCGGCGGCTGGCGTGTCTTCAT 1620  
QY 1621 GCTGTGTGTCAATGCCATGTGTGTACAGAGGGGGGTTTGAAGCTGTGTGACTGAG 1680  
|||||  
Db 1621 GCTGTGTGTCAATGCCATGTGTGTACAGAGGGGGGTTTGAAGCTGTGTGACTGAG 1680  
QY 1681 TACAGGAGACAGCTGACACCTACAGAGTGGGACATTAACCCGAGGATGAAGATCTAC 1740  
|||||  
Db 1681 TACAGGAGACAGCTGACACCTACAGAGTGGGACATTAACCCGAGGATGAAGATCTAC 1740  
QY 1741 ATCGATCTCTTCACTACAGAGACCCCAAGAGAGAGAGGAGTTTGGCAAGGAAT 1800  
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Db 1741 ATCGATCTCTTCACTACAGAGAGACCCCAAGAGAGAGAGGAGTTTGGCAAGGAAT 1800  
QY 1801 GACATCTCTGTGTCAAAATGTGAGAGGTTGAGAGAGAGGAGTTTGGCAAGGCTCTG 1860  
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Db 1801 GACATCTCTGTGTCAAAATGTGAGAGGTTGAGAGAGAGGAGTTTGGCAAGGCTCTG 1860

QY 1861 AGTGGCCACTGGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAGAGCCTTAC 1920  
|||||  
Db 1861 AGTGGCCACTGGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAGAGCCTTAC 1920  
QY 1921 TCGGGCTACAGGAG 1980  
|||||  
Db 1921 TCGGGCTACAGGAG 1980  
QY 1981 TTGACACATCCCAAGCTGATCAGCTGAGAGGCTGTGTGACCAAGAGACAGCTGTGATG 2040  
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Db 1981 TTGACACATCCCAAGCTGATCAGCTGAGAGGCTGTGTGACCAAGAGACAGCTGTGATG 2040  
QY 2041 ATCATCAACAGCTTCAAG 2100  
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Db 2041 ATCATCAACAGCTTCAAG 2100  
QY 2101 CAGTTCAAGTCAATCAAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGAGTAC 2160  
|||||  
Db 2101 CAGTTCAAGTCAATCAAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGAGTAC 2160  
QY 2161 CTGGACACATGAATATATTTACACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 2220  
|||||  
Db 2161 CTGGACACATGAATATATTTACACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 2220  
QY 2221 AACCTGTGTCAAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2280  
|||||  
Db 2221 AACCTGTGTCAAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2280  
QY 2281 GACCCACCTACACAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2340  
|||||  
Db 2281 GACCCACCTACACAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2340  
QY 2341 GCCATCAGTACAGGAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2400  
|||||  
Db 2341 GCCATCAGTACAGGAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2400  
QY 2401 TGGAGGTGATGTCTATGTGGGAGGCGGCTTACTGTGGGAGTGTGGGAGTGTGGGAGTGT 2460  
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Db 2401 TGGAGGTGATGTCTATGTGGGAGGCGGCTTACTGTGGGAGTGTGGGAGTGTGGGAGTGT 2460  
QY 2461 AATGCCATTGAGAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2520  
|||||  
Db 2461 AATGCCATTGAGAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2520  
QY 2521 CAATCATGTGTGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2580  
|||||  
Db 2521 CAATCATGTGTGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGT 2580  
QY 2581 GTCAACAGCTGAGCAAGATGTATCCCAATCCCAACAGGCTCAAAAGCCATGGCGCCCTC 2640  
|||||  
Db 2581 GTCAACAGCTGAGCAAGATGTATCCCAATCCCAACAGGCTCAAAAGCCATGGCGCCCTC 2640  
QY 2641 TCCCTGTGATCACTGCTGCGGCTGTGGAGCCGACAGATCCCGATCAACGAGTTTAA 2700  
|||||  
Db 2641 TCCCTGTGATCACTGCTGCGGCTGTGGAGCCGACAGATCCCGATCAACGAGTTTAA 2700  
QY 2701 ACAGTGTGAGAGTGTGTGGAGGCAATCAAGATGGGAGTGTGAAGAGAGTGTGGAGT 2760  
|||||  
Db 2701 ACAGTGTGAGAGTGTGTGGAGGCAATCAAGATGGGAGTGTGAAGAGAGTGTGGAGT 2760  
QY 2761 GCGGCTTACCTCTTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820  
|||||  
Db 2761 GCGGCTTACCTCTTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820  
QY 2821 GGGGCTACTTGTGGGCGGAGCAAGAAAAATTCGAACAGTATCCAGTGTGTGTGTGTGT 2880  
|||||  
Db 2821 GGGGCTACTTGTGGGCGGAGCAAGAAAAATTCGAACAGTATCCAGTGTGTGTGTGTGT 2880  
QY 2881 CAGATGAACAGATTCAGT 2940  
|||||  
Db 2881 CAGATGAACAGATTCAGT 2940  
QY 2941 CTCCAAGCCCGCCCTCTCTG 2962

Db 2941 CTCGAGCCCGCCCTCTGCG 2962

RESULT 3  
PCT-US95-04681-10

Sequence 10, Application PC/TUS9504681  
GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBM

STREET: 1840 Dehaven Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04681

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2962 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2913

PCT-US95-04681-10

Query Match

Best Local Similarity 100.0%; Score 2962; DB 5; Length 2962;

Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTGCTGCGCGCGGTGAGAAACGCTAATGACTCCACTACAGCGACTGCTGAGCTGGC 60  
1 CTGCTGCGCGCGGTGAGAAACGCTAATGACTCCACTACAGCGACTGCTGAGCTGGC 60  
61 TGGATGCTGATCTCTCATCAGAGGTGGAGAGGTAGTGGCTACGATGAACATGAAC 120  
61 TGGATGCTGATCTCTCATCAGAGGTGGAGAGGTAGTGGCTACGATGAACATGAAC 120  
121 AGCATCCGACGTCACCAAGGTGTGCAACGTTGAGTCAAGCAGAACTGGCTACAG 180  
121 AGCATCCGACGTCACCAAGGTGTGCAACGTTGAGTCAAGCAGAACTGGCTACAG 180  
181 ACCAAGTTATCCGGCGCGGTGGGCGCCACCGCATCCAGCTGAGATGAAGTTTGGTG 240  
181 ACCAAGTTATCCGGCGCGGTGGGCGCCACCGCATCCAGCTGAGATGAAGTTTGGTG 240  
241 CGTACTGCGACGATCCCGACGTCGCTGCTGCAAGAGACCTTCAACCTCTAT 300  
241 CGTACTGCGACGATCCCGACGTCGCTGCTGCAAGAGACCTTCAACCTCTAT 300  
301 TACTATGAGGCTGACTTTGACTGCGCCACCAAGACCTTCCCAACTGATGGAATCCA 360  
301 TACTATGAGGCTGACTTTGACTGCGCCACCAAGACCTTCCCAACTGATGGAATCCA 360  
361 TGGGTGAAGGTGATACCATTCGACGCCGACGAGAGCTTCTCCAGGTGGACTGGGTGGC 420

Db 361 TGGGTGAAGGTGATACCATTCGACGCCGACGAGAGCTTCTCCAGGTGGACTGGGTGGC 420  
421 CGCGTCATGAAATCAACACCGAGGTGCGAGCTTCGAGCTGTGTCGCCAGCGGCTTC 480  
421 CGCGTCATGAAATCAACACCGAGGTGCGAGCTTCGAGCTGTGTCGCCAGCGGCTTC 480  
481 TACCTGCTTCGACGATATGAGGTGGGTGATGCTGCTGATGCTGCTGCTGCTGCT 540  
481 TACCTGCTTCGACGATATGAGGTGGGTGATGCTGCTGATGCTGCTGCTGCTGCT 540  
541 CGCAAGTGGCGCGCATCATCAGATGAGGCGCATCTTCCAGAAACCTGTGCGGGGCT 600  
541 CGCAAGTGGCGCGCATCATCAGATGAGGCGCATCTTCCAGAAACCTGTGCGGGGCT 600  
601 GAGAGCATATGCTGTGCTGCTGCGGGGCGCATCTGCTGCTGCTGCTGCTGCTGCT 660  
601 GAGAGCATATGCTGTGCTGCTGCGGGGCGCATCTGCTGCTGCTGCTGCTGCTGCT 660  
661 GTACCATCAAGCTCTACTGTAACGCGGACGCGCATGCTGCTGCTGCTGCTGCTGCT 720  
661 GTACCATCAAGCTCTACTGTAACGCGGACGCGCATGCTGCTGCTGCTGCTGCTGCT 720  
721 ATGTGCAAGAGAGGCTTGAAGGCGGTGAGATGAGACCGCTGCTGCTGCTGCTGCT 780  
721 ATGTGCAAGAGAGGCTTGAAGGCGGTGAGATGAGACCGCTGCTGCTGCTGCTGCT 780  
781 GGGACTTTCAGAGGCGCAACCAAGGGGATGAGGCTGTACCCACTGTCCATCAACGCCG 840  
781 GGGACTTTCAGAGGCGCAACCAAGGGGATGAGGCTGTACCCACTGTCCATCAACGCCG 840  
841 ACCACTTTCAGAGGCGCGCAACCTGTGCTGCGGCAATGCTGCTGCTGCTGCTGCT 900  
841 ACCACTTTCAGAGGCGCGCAACCTGTGCTGCGGCAATGCTGCTGCTGCTGCTGCT 900  
901 GACCCCTGGAATGAGGCGCGCAACCTGTGCTGCGGCAATGCTGCTGCTGCTGCTGCT 960  
901 GACCCCTGGAATGAGGCGCGCAACCTGTGCTGCGGCAATGCTGCTGCTGCTGCTGCT 960  
961 GTCAATGAGAGCTTCCCTCATGCTGATGAGAGCCCTTCCCGGAGCTCGGAGGCCGAG 1020  
961 GTCAATGAGAGCTTCCCTCATGCTGATGAGAGCCCTTCCCGGAGCTCGGAGGCCGAG 1020  
1021 GACCTGCTCTACACATATCTGCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
1021 GACCTGCTCTACACATATCTGCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
1081 TGGGGGGAATGTACAGTACGACGACGCGCATGAGCTGAGCGACGACGATTTAC 1140  
1081 TGGGGGGAATGTACAGTACGACGACGCGCATGAGCTGAGCGACGACGATTTAC 1140  
1141 ATCAGTGAAGCTGCTGCGCCACACCGCATGACCTTCAAGATCCAGGCTGTGAACGGCGTT 1200  
1141 ATCAGTGAAGCTGCTGCGCCACACCGCATGACCTTCAAGATCCAGGCTGTGAACGGCGTT 1200  
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1201 ACTGACAGAGCCCTTCTGCGCTCAAGTTGCGCTGTGACATACCAACCAAGGCA 1260  
1261 GGTCCATGGGAGTGTGTCATGATGATGAGTGGCGCGCATGCTGAGATGAGTACCTG 1320  
1261 GGTCCATGGGAGTGTGTCATGATGATGAGTGGCGCGCATGCTGAGATGAGTACCTG 1320  
1321 TCGTGGTCCACCGCGACCGCAATGCGGTGATCTGAGTATGAGCTGAGTACTAT 1380  
1321 TCGTGGTCCACCGCGACCGCAATGCGGTGATCTGAGTATGAGCTGAGTACTAT 1380  
1381 GAGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
1381 GAGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
1441 GGCCTCAAGAGCGGCGCATATGCTTCCAGGTGCGGCGACGATGCTGCGAGGCTAC 1500  
1441 GGCCTCAAGAGCGGCGCATATGCTTCCAGGTGCGGCGACGATGCTGCGAGGCTAC 1500

Db 1441 GGCCTCAAGCCGGGCGCCATCTATGTCTTCCAGTGGCGGCGACGCACTGTGGCAGGCTAC 1500  
QY 1501 GGGCGCTACAGCGGCAAGTGTACTTCCAGACCATAGACAGAAAGCGGACTACAGCAAGC 1560  
Db 1501 GGGCGCTACAGCGGCAAGTGTACTTCCAGACCATAGACAGAAAGCGGACTACAGCAAGC 1560  
QY 1561 ATCCAGGAGAAAGTGGCCACTATCATCGGCTCTCCGCGGCTGGCTGTCTCTCTCATTT 1620  
Db 1561 ATCCAGGAGAAAGTGGCCACTATCATCGGCTCTCCGCGGCTGGCTGTCTCTCTCATTT 1620  
QY 1621 GCTGTGGTGTATGCGCATGTGTGTATACAGAGCGGGGTTTGGAGCTGTCTCTCTGAG 1680  
Db 1621 GCTGTGGTGTATGCGCATGTGTGTATACAGAGCGGGGTTTGGAGCTGTCTCTCTGAG 1680  
QY 1681 TACACGCAAGCTGCAACACTATACACAGTGGCCACATATACCCAGGCAATGAATCTAC 1740  
Db 1681 TACACGCAAGCTGCAACACTATACACAGTGGCCACATATACCCAGGCAATGAATCTAC 1740  
QY 1741 ATCGATCTCTTACCTACAGAGAGCCCAAGAGGCAAGTGGCGGAGTTTCCCAAGAAATT 1800  
Db 1741 ATCGATCTCTTACCTACAGAGAGCCCAAGAGGCAAGTGGCGGAGTTTCCCAAGAAATT 1800  
QY 1801 GACATCTCTGTGTCAAAATTTGAGAGGTGTATCGAGAGGCGGAGTTTGGGAGGCTGCG 1860  
Db 1801 GACATCTCTGTGTCAAAATTTGAGAGGTGTATCGAGAGGCGGAGTTTGGGAGGCTGCG 1860  
QY 1861 AGTGGCCACTGTAAGCTGCCAGGCAAGAGAGATCTTTTGGCGCATCAAGAGCTCAAG 1920  
Db 1861 AGTGGCCACTGTAAGCTGCCAGGCAAGAGAGATCTTTTGGCGCATCAAGAGCTCAAG 1920  
QY 1921 TCGGGCTACAGGAGAAAGCGGCGGAGCTCTCTGAGCGCAAGGCTCATCATCTGGGCGAG 1980  
Db 1921 TCGGGCTACAGGAGAAAGCGGCGGAGCTCTCTGAGCGCAAGGCTCATCATCTGGGCGAG 1980  
QY 1981 TTGACCATCCCAAGCTATCATCACTGGAGGAGTGTCTGACCAAGAGCACACCTGTGATG 2040  
Db 1981 TTGACCATCCCAAGCTATCATCACTGGAGGAGTGTCTGTGACCAAGAGCACACCTGTGATG 2040  
QY 2041 ATCTATCCAGGATCATGAGAGATGCTCTCCCTGTGAGCTCTTCTCCGCGCAAAAGCATGGG 2100  
Db 2041 ATCTATCCAGGATCATGAGAGATGCTCTCCCTGTGAGCTCTTCTCCGCGCAAAAGCATGGG 2100  
QY 2101 CAGTTTACAGTATCATGAGTGTGGGAGTGTGGGCGATCTGGGCGATTCGAGTGCATGAATAC 2160  
Db 2101 CAGTTTACAGTATCATGAGTGTGGGAGTGTGGGCGATCTGGGCGATTCGAGTGCATGAATAC 2160  
QY 2161 CTGGCAGACATGAATGTATGTTCACCGTGCCTGGCTGCCGCAACATCTCGTCAACAGC 2220  
Db 2161 CTGGCAGACATGAATGTATGTTCACCGTGCCTGGCTGCCGCAACATCTCGTCAACAGC 2220  
QY 2221 AACCTGGTGGCAAGGTGTGGGAGTGTGGGCTGTCAAGCTTTTCTAGAGAGCATACTCA 2280  
Db 2221 AACCTGGTGGCAAGGTGTGGGAGTGTGGGCTGTCAAGCTTTTCTAGAGAGCATACTCA 2280  
QY 2281 GACCCCACTACACAGTGTCTGGGCGGAAAGTTCCCAATCCGCTGGAGAGAGCCCGGAA 2340  
Db 2281 GACCCCACTACACAGTGTCTGGGCGGAAAGTTCCCAATCCGCTGGAGAGAGCCCGGAA 2340  
QY 2341 GCCATCCAGTACCGGAATTCACCTGGCGCAGTGTGTGAGCTACCGCATTTGTATG 2400  
Db 2341 GCCATCCAGTACCGGAATTCACCTGGCGCAGTGTGTGAGCTACCGCATTTGTATG 2400  
QY 2401 TGGGAGGTGATGCTATGGGAGGCGGCTTACTGGGAGATGACCAACAGATGTAAATC 2460  
Db 2401 TGGGAGGTGATGCTATGGGAGGCGGCTTACTGGGAGATGACCAACAGATGTAAATC 2460  
QY 2461 AATGCCATTGAGCAGACTATCGGCTGCCACCGCCATGAGAGCGCGGAGCGGCTGCAC 2520  
Db 2461 AATGCCATTGAGCAGACTATCGGCTGCCACCGCCATGAGAGCGCGGAGCGGCTGCAC 2520  
QY 2521 CAATCTATGCTGAGCTGTGGGAGGAAGAGACCGAACACCGGCGCAAGTTTGGCGCAAAAT 2580  
Db 2521 CAATCTATGCTGAGCTGTGGGAGGAAGAGACCGAACACCGGCGCAAGTTTGGCGCAAAAT 2580

QY 2581 GTCAACAGCTAGACCAAGATGATCCGCAATCCCAACAGCTCAAAAGCCATGGGCGCCCTC 2640  
Db 2581 GTCAACAGCTAGACCAAGATGATCCGCAATCCCAACAGCTCAAAAGCCATGGGCGCCCTC 2640  
QY 2641 TCCCTGTGCAATCAACCTGCGCTGCTGAGCGGCGACGATCCCGGCTACTACAGCTTAAAC 2700  
Db 2641 TCCCTGTGCAATCAACCTGCGCTGCTGAGCGGCGACGATCCCGGCTACTACAGCTTAAAC 2700  
QY 2701 ACGGTGACAGTGTGGTGGAGAGCCCATCAAGATGGGCGAGTACAAAGAGAGCTTGGCCAAAT 2760  
Db 2701 ACGGTGACAGTGTGGTGGAGAGCCCATCAAGATGGGCGAGTACAAAGAGAGCTTGGCCAAAT 2760  
QY 2761 GCGGGCTTCACTTCCCTTGTGAGCGTGTCTCAAGATGATGATGAGAGGATTTCCGGGTT 2820  
Db 2761 GCGGGCTTCACTTCCCTTGTGAGCGTGTCTCAAGATGATGATGAGAGGATTTCCGGGTT 2820  
QY 2821 GGGGTCACTTTGGCTGGCGCACAGAAAAAAATCCTGAACAGTATCCAGGTGATGGCGGCG 2880  
Db 2821 GGGGTCACTTTGGCTGGCGCACAGAAAAAAATCCTGAACAGTATCCAGGTGATGGCGGCG 2880  
QY 2881 CAGATGAACCAAGATTCAGTGTGTGGAGGTTTGAACATTCACCTGCTCGCTCACTCTTC 2940  
Db 2941 CTTCAAGCCCGCGCCCTCTGCG 2962  
QY 2941 CTTCAAGCCCGCGCCCTCTGCG 2962  
Db 2941 CTTCAAGCCCGCGCCCTCTGCG 2962

RESULT 4  
US-08-635-1  
; Sequence 1, Application US/08542635  
; Patent No. 6218356  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeier, Mark  
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
; NUMBER OF INVENTIONS: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bereskin & Parr  
; STREET: 40 King Street West, Box 401  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,635  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDiarmid, Shona S.  
; REGISTRATION NUMBER: 38,798  
; REFERENCE/DOCKET NUMBER: 3153-162  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; TELEX: 06-23115  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3105 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:

ORGANISM: Mus musculus  
DEVELOPMENTAL STAGE: Embryo  
IMMEDIATE SOURCE:  
LIBRARY: lambda gt10 cDNA library  
CLONE: combined PHUKACE A2 and K2 AND cDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Distal end of chromosome 4  
MAP POSITION: near the abd-1 mutation  
US-08-542-635-1

Query Match 1.6%; Score 48; DB 4; Length 3105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1440 GGGCCCAAGCCGGCCATCATCTCTCCAGCGGGGCGAC 1487  
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Db 1512 GGGCCTCAAGCCGGCCATCATCTCTCCAGGTGGGCGAC 1559

## RESULT 5

US-08-469-537A-28  
Sequence 28, Application US/08469537A  
Patent No. 5843749  
GENERAL INFORMATION:  
APPLICANT: Maisongier, et al.  
TITLE OF INVENTION: EHK AND ROR TYROSINE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/406,247  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: USN 08/144,992  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USN 07/736,559  
FILING DATE: 26-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempier, Ph.D., Gall M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 070C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
TELEX:  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..162  
US-08-469-537A-28

Query Match 1.2%; Score 35; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2206 ATCTGTCAACAGCACTGTGTGCAAGTGTG 2240  
|||||  
Db 1 ATCTGTCAACAGCACTGTGTGCAAGTGTG 35

## RESULT 6

US-08-162-809-7  
Sequence 7, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereydoon G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3776 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 290..3208  
US-08-162-809-7

Query Match 1.1%; Score 32; DB 1; Length 3776;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2389 GGCATTGTCTGGAGAGTGATGCTATG 2420  
|||||  
Db 2687 GGCATTGTCTGGAGAGTGATGCTATG 2718

## RESULT 7

US-08-162-809-1  
Sequence 1, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereydoon G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26



CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162.809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3133 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(3..419, 421..2858)  
US-08-162-809-1

Query Match 1.0%; Score 29; DB 1; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GGCTCTGCGAGAGACCTTCACCTCTA 299  
|||||  
DB 255 GGCTCTGCGAGAGACCTTCACCTCTA 283

RESULT 8  
US-08-469-537A-100  
Sequence 100, Application US/08469537A  
Patent No. 5843749  
GENERAL INFORMATION:  
APPLICANT: Maisongier, et al.  
TITLE OF INVENTION: EHK AND ROR TYROSINE  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/406,247  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: USSN 08/144,992

FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USSN 07/736,559  
FILING DATE: 26-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempler, Ph.D., Gail M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 070C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3592 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 598..3444  
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NAME/KEY: modified\_base  
LOCATION: 56  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /label= N  
OTHER INFORMATION: /note= "Where N = G, A, C or T"  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 3538  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /label= N  
OTHER INFORMATION: /note= "Where N = G, A, C or T"  
US-08-469-537A-100

Query Match 1.0%; Score 29; DB 2; Length 3592;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2392 ATTGTCATGTGGAGAGGTGATGCTATGG 2420  
|||||  
DB 3184 ATTGTCATGTGGAGAGGTGATGCTATGG 3212

RESULT 9  
US-08-162-809-17  
Sequence 17, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4049 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..2994  
US-08-162-809-17

Query Match 1.0%; Score 29; DB 1; Length 4049;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2212 GTCAACGACCACTGCTGTGCAAGGTGC 2240  
DB 2296 GTCAACGACCACTGCTGTGCAAGGTGC 2324

RESULT 10  
US-08-162-809-11  
Sequence 11, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereydoun G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4097 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..3042  
US-08-162-809-11

Query Match 1.0%; Score 29; DB 1; Length 4097;  
Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2212 GTCAACGACCACTGCTGTGCAAGGTGC 2240  
DB 2344 GTCAACGACCACTGCTGTGCAAGGTGC 2372

RESULT 11  
US-08-449-645A-23/c  
Sequence 23, Application US/08449645A  
Patent No. 5981245  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wintler, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-449-645A-23

Query Match 0.8%; Score 25; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1549 TACACGACATCCAGGAGACT 1573  
DB 39 TACACGACATCCAGGAGACT 15

RESULT 12  
US-08-702-367A-23/c  
Sequence 23, Application US/08702367A  
Patent No. 5981246  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ. ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-702-367A-23

Query Match 0.8%; Score 25; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 TACCAGACAAGCATCCAGAGAACT 1573  
|||||

DB 39 TACCAGACAAGCATCCAGAGAACT 15

RESULT 13  
PCT-US95-04681-23/c  
Sequence 23, Application PC/TUS9504681  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ. ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-04681-23

Query Match 0.8%; Score 25; DB 5; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 TACCAGACAAGCATCCAGAGAACT 1573  
|||||

DB 39 TACCAGACAAGCATCCAGAGAACT 15

RESULT 14  
US-08-469-537A-65  
Sequence 65, Application US/08469537A  
Patent No. 5843749  
GENERAL INFORMATION:  
APPLICANT: Maisondier, et al.  
TITLE OF INVENTION: EHK AND FOR TYROSINE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneration Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/406,247  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: USSN 08/144,992  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USSN 07/736,559  
FILING DATE: 26-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempler, Ph.D., Gail M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 070C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
TELEX:  
INFORMATION FOR SEQ. ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..81  
US-08-469-537A-65

Query Match 0.8%; Score 25; DB 2; Length 81;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2180 TTCACCGTGACCTGGCTGCCGCAA 2204  
|||||

DB 11 TTCACCGTGACCTGGCTGCCGCAA 35

RESULT 15  
US-08-162-809-9  
Sequence 9, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereyoun G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CAMPBELL AND FLORES  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/162,809  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 9503  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3546 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 2..2920  
;; US-08-162-809-9

Query Match 0.88; Score 25; DB 1; Length 3546;  
Best Local Similarity 100.0%; Pred. No. 0 012;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1163 CCCAGTACACCTTCGAGATCCAGGC 1187  
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Db 1176 CCCAGTACACCTTCGAGATCCAGGC 1200

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Perfect score: 2962  
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Scoring table: OLIGO\_NUC  
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Minimum DB seq length: 0

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148: gb_est187:*
149: gb_est188:*
150: gb_est189:*
151: gb_est190:*
152: gb_est199:*
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154: gb_est101:*
155: gb_est102:*
156: gb_est103:*
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159: gb_est106:*
160: gb_est167:*
161: gb_est168:*
162: gb_est169:*
163: gb_est170:*
164: gb_est171:*
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171: gb_est194:*
172: gb_est195:*
173: gb_est196:*
174: gb_est197:*
175: gb_est198:*
176: em_esthum29:*
177: em_esthum30:*
178: em_esthum31:*
179: em_esthum32:*
180: em_esthum33:*
181: em_estom3:*
182: em_estpl11:*
183: em_estro21:*
184: em_estro22:*
185: em_estro23:*
186: em_hlc:*
187: gb_est107:*
188: gb_est108:*
189: gb_est109:*

190: gb_est110:*
191: gb_est111:*
192: gb_hlc:*
193: em_gss_fun:*
194: em_gss_hum1:*
195: em_gss_hum2:*
196: em_gss_hum3:*
197: em_gss_hum4:*
198: em_gss_hum5:*
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200: em_gss_hum7:*
201: em_gss_hum8:*
202: em_gss_hum9:*
203: em_gss_inv1:*
204: em_gss_inv2:*
205: em_gss_inv3:*
206: em_gss_other:*
207: em_gss_pln1:*
208: em_gss_pln2:*
209: em_gss_pro:*
210: em_gss_rod1:*
211: em_gss_rod2:*
212: em_gss_rod3:*
213: em_gss_rod4:*
214: em_gss_rod5:*
215: em_gss_vrt1:*
216: em_gss_vrt2:*
217: em_gss_vrt3:*
218: gb_gss1:*
219: gb_gss2:*
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222: gb_gss5:*
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224: gb_gss7:*
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246: gb_gss29:*
247: gb_gss30:*
248: gb_gss31:*
249: gb_gss32:*
250: gb_gss33:*
251: gb_gss34:*
252: em_gss_inv4:*
253: em_gss_rod6:*
254: em_gss_rod7:*
255: em_gss_rod8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



QY 2380 TGGAGCTAC 2388  
|||||||  
Db 681 TGGAGCTAC 689

RESULT 2  
BE314746 769 bp mRNA EST 26-OCT-2000  
LOCUS 601148809F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3501578 5',  
DEFINITION mRNA sequence.  
ACCESSION BE314746  
VERSION BE314746.1 GI:9136248  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 769)  
NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM172 row: a column: 03  
High quality sequence start: 16  
High quality sequence stop: 683.  
Location/Qualifiers  
1. 769  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_11b="IMAGE:3501578"  
/clone\_11b="NIH\_MGC\_19"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pORF7; Site:1: XhoI; Site:2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."  
BASE COUNT 162 a 254 c 214 g 139 t

ORIGIN

Query Match 14.8%; Score 437; DB 166; Length 769;  
Best Local Similarity 99.8%; Pred. No. 3.7e-227;  
Matches 557; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 697 TGGCTGTGCGCCATCGGGGCGCTGATGCAAGCAGGCTTCAGAGCCGTGGAATGGC 756  
|||||||  
Db 61 TGGCTGTGCGCCATCGGGGCGCTGATGCAAGCAGGCTTCAGAGCCGTGGAATGGC 120

QY 757 ACCGTGTGCGAGGTGTCCATCTGGGACTTCAAGGCCAACCAAGGGATGAGGCTGT 816  
|||||||  
Db 121 ACCGTGTGCGAGGTGTCCATCTGGGACTTCAAGGCCAACCAAGGGATGAGGCTGT 180

QY 817 ACCCATGTGCCATCAACAGCCGAGCACTTCTGAAGGGGCGACCAACTGTGTGCGGC 876  
|||||||  
Db 181 ACCCATGTGCCATCAACAGCCGAGCACTTCTGAAGGGGCGACCAACTGTGTGCGGC 240

QY 877 AATGGCTACTAAGAGACAGCACTGGAGCCCGCTGGAGATGCCCTGCACATCCCTCC 936  
|||||||  
Db 241 AATGGCTACTAAGAGACAGCACTGGAGCCCGCTGGAGATGCCCTGCACATCCCTCC 300

QY 937 GCGCCCGAGGCTGTGATTTCCAGTGTCAATGAGACCTCCCTCATGCTGAGAGGACCCCT 996

Db 301 GCGCCCGAGGCTGTGATTTCCAGTGTCAATGAGACCTCCCTCATGCTGAGAGGACCCCT 360  
|||||||

QY 997 CCGCGAGACTCCGGA-GGCCGAGAGAGACCTCTGTACACATCATCTGCAGAGACTGTGG 1055  
|||||||

Db 361 CCGCGAGACTCCGAGATGGCCGAGAGACCTGTGTACACATCATCTGCAGAGACTGTGG 420  
|||||||

QY 1056 CTGCGGCCGGGGTCCCTGCACACCCCTCGGGGAGACATGTACAGACACCCAGCT 1115  
|||||||

Db 421 CTCGGCCGGGGTCCCTGCACACCCCTCGGGGAGACATGTACAGACACCCAGCT 480  
|||||||

QY 1116 AGGCTGACGAGC CAGGANTTTACATCATGAGACCTCTGGCCACACCCAGTACACTT 1175  
|||||||

Db 481 AGGCTGACGAGC CAGGANTTTACATCATGAGACCTCTGGCCACACCCAGTACACTT 540  
|||||||

QY 1176 CGAGATCCAGGCTGTGAAGCGCGCTTACTGACACGAGCCCTTCTCGCCTCAGTTGGCTC 1235  
|||||||

Db 541 CGAGATCCAGGCTGTGAAGCGCGCTTACTGACACGAGCCCTTCTCGCCTCAGTTGGCTC 600  
|||||||

QY 1236 TGTGAACATCACCAACCA 1253  
|||||||

Db 601 TGTGAACATCACCAACCA 618  
|||||||

RESULT 3  
BG425170 916 bp mRNA EST 14-MAR-2001  
LOCUS BG425170  
DEFINITION 60244663F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4585526 5',  
mRNA sequence.  
ACCESSION BG425170  
VERSION BG425170.1 GI:13331676  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 916)  
NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM1312 row: m column: 15  
High quality sequence stop: 726.  
Location/Qualifiers  
1. 916  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_11b="IMAGE:4585526"  
/clone\_11b="NIH\_MGC\_14"  
/tissue\_type="renal cell adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: kidney; Vector: pORF7; Site:1: XhoI; Site:2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 221 a 251 c 284 g 160 t

ORIGIN

Query Match 13.7%; Score 406; DB 153; Length 916;  
Best Local Similarity 99.7%; Pred. No. 3.4e-210;

Matches 576; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

OY 1489 GTGCGAGCTACGGGCGCTACAGCGCAAGATGTACTTCCAGACCATGACGAGCCGAG 1548
    |||||||
DB 7 GTGGAGGCTACGGGCGCTACAGCGCAAGATGTACTTCCAGACCATGACGAGCCGAG 66
    |||||||
OY 1549 TACGAGACACATCCAGGAGAGTTGGCACTCATCATCGGCTCTGGGCGCTGGCTG 1608
    |||||||
DB 67 TACGAGACACATCCAGGAGAGTTGGCACTCATCATCGGCTCTGGGCGCTGGCTG 126
    |||||||
OY 1609 GTCTTCTCATTTGCTGTGTGTATCGCCATCGTGTGTATACAGAGGGGGTTGAGCCT 1668
    |||||||
DB 127 GTCTTCTCATTTGCTGTGTGTATCGCCATCGTGTGTATACAGAGGGGGTTGAGCCT 186
    |||||||
OY 1669 GCTGACTGGAGTACAGCGAAGCTGCAACATACACATGCGGCACTAACCCGAGGC 1728
    |||||||
DB 187 GCTGACTGGAGTACAGCGAAGCTGCAACATACACATGCGGCACTAACCCGAGGC 246
    |||||||
OY 1729 ATGAAGATCTACATCATCTCTTTCACCTACGAGAGCCCAAGAGAGAGTGGAGTTT 1788
    |||||||
DB 247 ATGAAGATCTACATCATCTCTTTCACCTACGAGAGCCCAAGAGAGAGTGGAGTTT 306
    |||||||
OY 1789 GCCAAGAAATTTGACATCTCTCTGTCTCAAAATTTAGCAGGTGATCGAGAGGAGTTT 1848
    |||||||
DB 307 GCCAAGAAATTTGACATCTCTCTGTCTCAAAATTTAGCAGGTGATCGAGAGGAG-TT 365
    |||||||
OY 1849 GCGGAGGTCTGAGTGGGCGACCTGAAGCTGCGAGGCAAGAGAGATCTTTTGGCCATC 1908
    |||||||
DB 366 GCGGAGGTCTGAGTGGGCGACCTGAAGCTGCGAGGCAAGAGAGATCTTTTGGCCATC 425
    |||||||
OY 1909 AAGAGCTCAAGTGGGCTACACGAGAGAGAGAGCGCGGAGCTTCTGAGGAGAGCTTCC 1968
    |||||||
DB 426 AAGAGCTCAAGTGGGCTACACGAGAGAGAGAGCGCGGAGCTTCTGAGGAGAGCTTCC 485
    |||||||
OY 1969 ATCATGGGCGCACTTGGACCATCCCAAGCTCATCCACCTGGAGGGTGTGTGACCAAGGC 2028
    |||||||
DB 486 ATCATGGGCGCACTTGGACCATCCCAAGCTCATCCACCTGGAGGGTGTGTGACCAAGGC 545
    |||||||
OY 2029 ACACCTGTGATCATCATCAGGAGTTTCATGGAGAAATGG 2066
    |||||||
DB 546 ACACCTGTGATCATCATCAGGAGTTTCATGGAGAAATGG 583
    |||||||

```

RESULT 4  
 BE256685 523 bp mRNA EST 13-JUL-2000  
 LOCUS 60110774F1 NIH\_MGC\_16 Homo sapiens cDNA clone IMAGE:343843 5',  
 DEFINITION mRNA sequence.

ACCESSION BE256685  
 VERSION BE256685  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE NIH-MGC http://mhc.nci.nih.gov/  
 1 (bases 1 to 523)  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 plate: L1CM129 row: d column: 20  
 High quality sequence stop: 522.  
 Location/Qualifiers  
 1..523  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

FEATURES  
 source

```

/clone="IMAGE:343843"
/clone_lib="NIH_MGC_16"
/issue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pORF1; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGGCAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."
BASE COUNT 107 a 189 c 135 g 92 t
ORIGIN

```

Query Match 13.0%; Score 384; DB 165; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 971 CCTCCCTCATGCTGAGTGGAGTGGACCCCTCCCGCAGATCCGAGAGCGGAGAGACTGCTT 1030
    |||||||
DB 140 CCTCCCTCATGCTGAGTGGAGTGGACCCCTCCCGCAGATCCGAGAGCGGAGAGACTGCTT 199
    |||||||
OY 1031 ACAACATCATCTGCAAGAGCTGTGGCTGGCGCGGGGTGCTGTGACCCCTGGCGGGACA 1090
    |||||||
DB 200 ACAACATCATCTGCAAGAGCTGTGGCTGGCGCGGGGTGCTGTGACCCCTGGCGGGACA 259
    |||||||
OY 1091 ATGTACAGTATGACGACGAGGAGCTAGGAGCTGACGAGAGCCAGCATTTACATCAGTACC 1150
    |||||||
DB 260 ATGTACAGTATGACGACGAGGAGCTAGGAGCTGACGAGAGCCAGCATTTACATCAGTACC 319
    |||||||
OY 1151 TGCTGGCCACACCCAGTACACCTTTCAGATCCAGGCTGTGAAAGGCGTTACTGACAGA 1210
    |||||||
DB 320 TGCTGGCCACACCCAGTACACCTTTCAGATCCAGGCTGTGAAAGGCGTTACTGACAGA 379
    |||||||
OY 1211 GCCCCTTCTGCCCTCAGTTCCTCTGTGAAACATCACACCAACAGGAGGCTGATCGG 1270
    |||||||
DB 380 GCCCCTTCTGCCCTCAGTTCCTCTGTGAAACATCACACCAACAGGAGGCTGATCGG 439
    |||||||
OY 1271 CAGTGTCCATCATCATCAGTGGAGGCGCAGCGTGGAGAGCATTTACCTGTGTGTGCC 1330
    |||||||
DB 440 CAGTGTCCATCATCATCAGTGGAGGCGCAGCGTGGAGAGCATTTACCTGTGTGTGCC 499
    |||||||
OY 1331 AGCCGAGACAGCCCAATGGCGTGA 1354
    |||||||
DB 500 AGCCGAGACAGCCCAATGGCGTGA 523
    |||||||

```

RESULT 5  
 AM806532/c 588 bp mRNA EST 17-MAY-2000  
 LOCUS I10-ST0002-160599-012 ST0002 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION AM806532  
 ACCESSION AM806532  
 VERSION AM806532.1 GI:7899531  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 588)  
 Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-27049222  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?lib=62=IL0-ST0002-160-599-012&f3=1999-05-16&f4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 589.

## FEATURES

## SOURCE

Location/Qualifiers

1..588

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="ST0002"

/dev\_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## BASE COUNT

111 a 152 c 192 g 133 t

## ORIGIN

## Query Match

Best Local Similarity 12.4%; Score 366; DB 120; Length 588;

Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2141 TCGCAGCTGCATGAGTACCTGGCAGACATGAACTATGTTCACTGACCTGGCTGCC 2200  
|||||  
519 TCGCAGCTGCATGAGTACCTGGCAGACATGAACTATGTTCACTGACCTGGCTGCC 460  
|||||  
2201 GCAACATCTCTGTCACACACACACCTGCTGCAAGGTGCGACTTGGGCTCTCAGCCT 2260  
|||||  
459 GCAACATCTCTGTCACACACACACCTGCTGCAAGGTGCGACTTGGGCTCTCAGCCT 400  
|||||  
2261 TTCTAGAGAGAGATACCTGACACCCACACACACCTGCTGCGGGGAGAAAGTCCCA 2220  
|||||  
399 TTCTAGAGAGAGATACCTGACACCCACACACACCTGCTGCGGGGAGAAAGTCCCA 340  
|||||  
2321 TCCGCTGAGACGCCCGGAGACCATCAGTACCGGAAGTTACCTGCGGCAGTGTGT 2380  
|||||  
339 TCCGCTGAGACGCCCGGAGACCATCAGTACCGGAAGTTACCTGCGGCAGTGTGT 280  
|||||  
2381 GGAGCTACGGCATTTGTATGTGGAGGTGATGTCCTATGTGGGAGCGGCCCTACTGGACA 2440  
|||||  
279 GGAGCTACGGCATTTGTATGTGGAGGTGATGTCCTATGTGGGAGCGGCCCTACTGGACA 220  
|||||  
2441 TGACCAACACAGATGATATCATGATGAGAGAGACTATGCGGTGCCACGCCCATG 2500  
|||||  
219 TGACCAACACAGATGATATCATGATGAGAGAGACTATGCGGTGCCACGCCCATG 160  
|||||  
2501 ACTGCCGAGCGCCCTGACACCACTCATGCTGACTGTTGGCAGAAAGACCCGACACCC 2560  
|||||  
159 ACCGCCGAGCGCCCTGACACCACTCATGCTGACTGTTAGCAGAAAGACCCGACACCC 100  
|||||  
2561 GGCCCAAGTTCGGCCCAATTTGTCAACAGCTAGACAGATGATCCCAATCCCAACAGCC 2620  
|||||  
99 GGCCCAAGTTCGGCCCAATTTGTCAACAGCTAGACAGATGATCCCAATCCCAACAGCC 40  
|||||  
2621 TCAAAAGCATGGGCGCCCTCTCTCTGCGATCAACCTGC 2659  
|||||  
39 TCAAAAGCATGGGCGCCCTCTCTCTGCGATCAACCTGC 1

RESULT 6  
AL040428/c 800 bp mRNA EST 29-FEB-2000  
LOCUS AL040428 800 bp mRNA EST 29-FEB-2000

## DEFINITION

DKFZp434C1814.s1.434 (synonym: htes3) Homo sapiens cDNA clone

DKFZp434C1814.3', mRNA sequence.

## ACCESSION

AL040428.1 GI:5409379

## VERSION

EST.

## KEYWORDS

human.

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 800)

## AUTHORS

Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

## TITLE

EST (Koehler, et al.)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Koehler K

## MIPS

Am Kioferspitz 18a D-82152 Martinsried, Germany

## This is the 3' sequence of the clone insert

This is from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

## sequenced by BMFZ (Biomedical Research Center at the Charité, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

If sequence also available.

## This clone (DKFZp434C1814) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

## SOURCE

Location/Qualifiers

1..800

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="DKFZp434C1814"

/clone.lib="434 (synonym: htes3)"

/dev\_stage="adult"

/tissue\_type="testis"

/lab\_host="DH10B"

/note="Vector: pSPori1; Site\_1: NotI; Site\_2: SalI"

## BASE COUNT

193 a 223 c 198 g 186 t

## ORIGIN

## Query Match

Best Local Similarity 11.1%; Score 328; DB 105; Length 800;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

444 GGTGCGAGCTTGCGACCTGTGTCGCCGACGCGCTTCACTGGCCCTTCAGAGACTATGG 503  
|||||  
768 GTGCGGAGCTTGCGACCTGTGTCGCCGACGCGCTTCACTGGCCCTTCAGAGACTATGG 709  
|||||  
504 CGGCTCATGTCCCTCATGCGCGTGGTGTCTTACCGCAAGTGGCCCCGATATCCA 563  
|||||  
708 CGGCTCATGTCCCTCATGCGCGTGGTGTCTTACCGCAAGTGGCCCCGATATCCA 649  
|||||  
564 GAATGGCGCATCTTCCAGGAACCTGTGCGGGGTGAGACACATCGCTGTGGCTGC 623  
|||||  
648 GAATGGCGCATCTTCCAGGAACCTGTGCGGGGTGAGACACATCGCTGTGGCTGC 589  
|||||  
624 CCGGGGACAGCTCATGCGCAATGCGGAAGAGGTGATGATACCATCAAGCTTACTGTAA 683  
|||||  
588 CCGGGGACAGCTCATGCGCAATGCGGAAGAGGTGATGATACCATCAAGCTTACTGTAA 529  
|||||  
684 CCGGGGACAGCTCATGCGCAATGCGGAAGAGGTGATGATACCATCAAGCTTACTGTAA 743  
|||||  
528 CCGGGGACAGCTCATGCGCAATGCGGAAGAGGTGATGATACCATCAAGCTTACTGTAA 469  
|||||  
744 CGTGAAGATGGCACCGTCTGCGGAGGT 771  
|||||  
468 CGTGAAGATGGCACCGTCTGCGGAGGT 441

RESULT 7  
A1940301/c 325 bp mRNA EST 03-AUG-1999  
LOCUS A1940301 325 bp mRNA EST 03-AUG-1999  
DEFINITION CM2-CT0040-230799-001-A02 CT0040 Homo sapiens cDNA, mRNA sequence.

ACCESSION AT940301  
VERSION GI:5687282  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 325)  
AUTHORS HCCP <http://www.ludwig.org.br/ORESTES>.  
TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-CT0040-230799-001-A02&f3=1999-07-23&tl4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 325.  
Location/Qualifiers  
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BASE COUNT 58 a 85 c 104 g 78 t  
ORIGIN  
Query Match 10.9%; Score 323; DB 104; Length 325;  
Best Local Similarity 100.0%; Pred. No. 7,9e-165;  
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2335 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGAGATGTGGAGCTACGGCAT 2394  
DB 325 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGAGATGTGGAGCTACGGCAT 266  
OY 2395 GTCATGTGGAGGTGATGTCCTATGGGAGGCGCCCTACTGGAGATGACCAACGAGAT 2454  
DB 265 GTCATGTGGAGGTGATGTCCTATGGGAGGCGCCCTACTGGAGATGACCAACGAGAT 206  
OY 2455 GTAATCATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCCGAGCCG 2514  
DB 205 GTAATCATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCCGAGCCG 146  
OY 2515 CTGCACCACTCATCTGAGACTGTTGGCAGAAAGACCGCAACACCGGCCCAAGTTCCG 2574  
DB 145 CTGCACCACTCATCTGAGACTGTTGGCAGAAAGACCGCCCAAGTTCCG 86  
OY 2575 CAATTTGTCACACGCTAGACAAAGATGATCCGCAATCCCAACAGCCCTCAAAAGCCATGGCG 2634  
DB 85 CAATTTGTCACACGCTAGACAAAGATGATCCGCAATCCCAACAGCCCTCAAAAGCCATGGCG 26  
OY 2635 CCCCTCTCCTCTGGCATCAACT 2657  
DB 25 CCCCTCTCCTCTGGCATCAACT 3

LOCUS AM845008 448 bp mRNA EST 19-MAY-2000  
DEFINITION RC0-CP0002-310599-003 CT0002 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM845008  
VERSION AM845008.1 GI:7940434  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 448)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zaio,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL MEDLINE  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC0-CT0002-310599-003&f3=1999-05-31&tl4=1>)  
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High quality sequence start: 12  
High quality sequence stop: 387.  
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/clone\_lib="CT0002"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 81 a 116 c 143 g 106 t 2 others  
ORIGIN  
Query Match 10.9%; Score 323; DB 121; Length 448;  
Best Local Similarity 100.0%; Pred. No. 8,1e-165;  
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2335 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGAGATGTGGAGCTACGGCAT 2394  
DB 325 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGAGATGTGGAGCTACGGCAT 266  
OY 2395 GTCATGTGGAGGTGATGTCCTATGGGAGGCGCCCTACTGGAGATGACCAACGAGAT 2454  
DB 265 GTCATGTGGAGGTGATGTCCTATGGGAGGCGCCCTACTGGAGATGACCAACGAGAT 206  
OY 2455 GTAATCATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCCGAGCCG 2514  
DB 205 GTAATCATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCCGAGCCG 146  
OY 2515 CTGCACCACTCATCTGAGACTGTTGGCAGAAAGACCGCAACACCGGCCCAAGTTCCG 2574  
DB 145 CTGCACCACTCATCTGAGACTGTTGGCAGAAAGACCGCCCAAGTTCCG 86  
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Db      85  CAAATGTCAACAGCTAGACAGATGATCGCATCCCAACAGCTCAAGCATGGCG 26
      2635 CCGCTCTCTCTGGCATCAACCT 2657
      25  CCGCTCTCTCTGGCATCAACCT 3

RESULT  9
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LOCUS     FM3-DT0064-260300-002-f08 DT0064 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AM938783
VERSION    AM938783.1 GI:8114229
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 517)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
          Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
          Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
          ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
          Simpson,A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL   20202663
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COMMENT   Laboratory of Cancer Genetics
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          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?l=642-FM3-DT0064-260
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          Seq primer: puc 18 forward
          High quality sequence stop: 514.
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              /clone_lib="DT0064"
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              /note="Organ: denis.drash; Vector: puc18; Site_1: SmaI;
              Site_2: SmaI; A mini-library was made by cloning products
              derived from ORESTES PCR (U.S. Letters Patent application
              No. 196,716 - Ludwig Institute for Cancer Research)
              profiles into the pUC 18 vector. Reverse transcription of
              tissue mRNA and cDNA amplification were performed under
              low stringency conditions."
              Location/Qualifiers
                BASE COUNT 97 a 133 c 168 g 119 t
                ORIGIN
                Query Match 10.4%; Score 307; DB 122; Length 517;
                Best Local Similarity 99.2%; Pred. No. 4,6e-156;
                Matches 507; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2141 TCGCAGCTGGCATGAGTACTGGCAGACATGATGTTCCACCGTGGCTGGCC 2200
      517 TCGCAGCTGGCATGAGTACTGGCAGACATGATGTTCCACCGTGGCTGGCC 458
      2201 GCAACATCTCTGTCACAGCAACCTGCTGCGAAGGTGTGGACTTTGGCTCTACGCT 2260
      457 GCAACATCTCTGTCACAGCAACCTGCTGCGAAGGTGTGGACTTTGGCTCTACGCT 398
  
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QY      2261 TTCTAGAGAGATNACTCTACAGCCACCTACACCACTGCTGGCGGAAGTTC 2320
      397 TTCTAGAGAGATNACTCTACAGCCACCTACACCACTGCTGGCGGAAGTTC 338
      2321 TCGCGTGACAGCCCGGAAAGCATTCAGTACGGAAGTTACCTGGCGAGTGTGT 2380
      337 TCGCGTGACAGCCCGGAAAGCATTCAGTACGGAAGTTACCTGGCGAGTGTGT 278
      2381 GGAGCTACGCATTTGATGATGAGTGTGATGTCCTTGGGGAGCGGCCCTACTGGGACA 2440
      277 GGAGCTACGCATTTGATGATGAGTGTGATGTCCTTGGGGAGCGGCCCTACTGGGACA 218
      2441 TGACCAACAGAGATGTATATCATGATGATGAGCAGCATATTCGGCTGCCACCCCATG 2500
      217 TGACCAACAGAGATGTATATCATGATGATGAGCAGCATATTCGGCTGCCACCCCATG 158
      QY      2501 ACTGCGGAGCGCCCTGACCACTATGCTGTGAGCTTTGGCAGAGAGCCGACCAACC 2560
      157 ACTGCGGAGCGCCCTGACCACTATGCTGTGAGCTTTGGCAGAGAGCCGACCAACC 98
      QY      2561 GGGCCAGTTGCGGCAATGTCACACGCTAGACAGATGATCCGATCCGACAGCC 2620
      97 GGGCCAGTTGCGGCAATGTCACACGCTAGACAGATGATCCGATCCGACAGCC 38
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      37 TCAAGGCATGCGCGCCCTCTCTCTGGCAT 7

RESULT  10
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LOCUS     601893088F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138988 5',
DEFINITION
ACCESSION BF306234
VERSION    BF306234.1 GI:11253319
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs@email.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
          Plate: LILCM1048 row: o column: 21
          High quality sequence stop: 646.
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              /db_xref="taxon:9606"
              /clone_lib="IMAGE:4138988"
              /clone_lib="NIH_MGC_17"
              /tissue_type="rhabdomyosarcoma"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
              Site_2: XhoI; CDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(5). Size-selected >500bp
              for average insert size 1.8kb. Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).".
              Location/Qualifiers
                BASE COUNT 214 a 261 c 297 g 166 t
                ORIGIN
  
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Query Match 10.18; Score 300; DB 147; Length 939;  
 Best Local Similarity 99.68; Pred. No. 3.2e-152;  
 Matches 470; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

36 CACTACACGAGCTGCTGAGCTGGGCTGGATGCTCCTCATCAGAGGAGGAGAGT 95  
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 Db 2 CACTACACGAGCTGCTGAGCTGGGCTGGATGCTCCTCATCAGAGGAGGAGT 61  
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96 GAGTGGCTACGATGAGACATGACACGATCCGACGATACAGAGTGTCAAGTGTGA 155  
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 Db 62 GAGTGGCTACGATGAGACATGAGACGATCCGACGATACAGAGTGTCAAGTGTGA 121  
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156 GTCAAGCCAGAACACTGGCTACGACCAAGTTTATCCGGGGCCCTGGGGCCACCGCAT 215  
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 Db 122 GTCAAGCCAGAACACTGGCTACGACCAAGTTTATCCGGGGCCCTGGGGCCACCGCAT 181  
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216 CCACGTGGAGATGAGATTTTGGCTGCTGACCTGACGACGACATCCCGACGCTGGCTC 275  
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 Db 182 CCACGTGGAGATGAGATTTTGGCTGCTGACCTGACGACGACATCCCGACGCTGGCTC 241  
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276 CTGCAAGAGAGACTTCAACCTCTATTACTATGAGGCTGACTGCTGGCC-CACCAAGA 334  
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 Db 242 CTGCAAGAGAGACTTCAACCTCTATTACTATGAGGCTGACTGCTGGCC-CACCAAGA 301  
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335 CCTTCCCAACCTGATGAGATGAGATGAGGATGAGATGAGATGAGATGAGATGAGAT 394  
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 Db 302 CCTTCCCAACCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 361  
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395 GCTTCTCCAGGTGAGACTGCTGGTGGCCGCTGATGAAATCAACACCGAGTGGGAGCT 454  
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 Db 362 GCTTCTCCAGGTGAGACTGCTGGTGGCCGCTGATGAAATCAACACCGAGTGGGAGCT 421  
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455 TGGGACCTGTGTCCGACACGCTTCTACTGGCTTCCAGAGATATGGCGG 506  
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 Db 422 TGGGACCTGTGTGTCCGACACGCTTCTACTGGCTTCCAGAGATATGGCGG 473  
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RESULT 11  
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 LOCUS lb98b01.x1 NCI-CGAP.Col6 Homo sapiens cDNA clone IMAGE:2062345.3  
 DEFINITION similar to SW:EP82\_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR  
 ; contains element MER22 repetitive element ; mRNA sequence..  
 A1337308  
 ACCESSION A1337308.1 GI:4074235  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 496)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-ri@mail.nih.gov  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.  
 , Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.dlo.llnl.gov/bdrp/image/image.html  
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 /lab\_host="DH10B"  
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Plasmid DNA from the normalized library NCI-CGAP.Col6 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clones 1057416-1061251, and 1144584-1145351).  
 Subtraction by Bento Soares and M. Fatima Bonaldo.  
 BASE COUNT 104 a 141 c 148 g 103 t  
 ORIGIN

Query Match 9.98; Score 292; DB 19; Length 496;  
 Best Local Similarity 99.78; Pred. No. 7.4e-148;  
 Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 GTTGTAGTCAAGCCAGAACACTGGCTACGACCAAGTTTATCCGGGCGCTGGGGCCA 60  
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210 CCGCATCCACGCTGAGATGAGATGAGTTTGGTGGTGGTACTGACAGACATCCCGACGTC 269  
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 Db 61 CCGCATCCACGCTGAGATGAGATGAGTTTGGTGGTGGTACTGACAGACATCCCGACGTC 120  
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270 TGGCTCTGCAAGAGAGACTTCAACCTCTATTACTATGAGGCTACATTGACTGGGCCAC 329  
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 Db 121 TGGCTCTGCAAGAGAGACTTCAACCTCTATTACTATGAGGCTACATTGACTGGGCCAC 180  
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330 CAAGACTTCCCAACCTGATGAGATGAGATGAGTGGTGAAGTGATACATTGACGCCGA 389  
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 Db 181 CAAGACTTCCCAACCTGATGAGATGAGATGAGTGGTGAAGTGATACATTGACGCCGA 240  
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390 CGAGAGCTTCTCCAGGTGAGCTGGTGGCCGCTCATGAAATCAACACCGAGTGGC 449  
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 Db 241 CGAGAGCTTCTCCAGGTGAGCTGGTGGCCGCTCATGAAATCAACACCGAGTGGC 300  
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450 GAGCTTCCGACCTGTGTCCCGAGCGGCTTACTTGGCCTTC 492  
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 Db 301 GAGCTTCCGACCTGTGTCCCGAGCGGCTTACTTGGCCTTC 343  
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RESULT 12  
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 DEFINITION similar to SW:EP82\_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR  
 ; mRNA sequence.  
 A1828089  
 ACCESSION A1828089.1 GI:5448760  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 687)  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-ri@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.



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Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
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Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=CM1&t2=CM1-NN0193-  
251000-485-d08&t3=2000-10-25&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 46  
High quality sequence stop: 445.  
Location/Qualifiers

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/note="Organ: nervous\_normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT  
111 a 149 c 112 g 73 t  
ORIGIN

Query Match 9.0% Score 268; DB 171; Length 445;  
Best Local Similarity 99.5%; Pred. No. 9.8e-135;  
Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2315 TCCCATCCGCTGACACACCCCGAAGCCATCAGTACCGAAGTTCACCTGGCCAGTG 2374  
DB 57 TCCCATCCGCTGACACACCCCGAAGCCATCAGTACCGAAGTTCACCTGGCCAGTG 116  
2375 ATGTGTGAGCTACGCGATGTGTATGTGGAGAGTATCTCTATGGGAGCGCCCTACT 2434  
DB 117 ATGTGTGAGCTACGCGCTTGTATGTGGAGAGTATCTCTATGGGAGCGCCCTACT 176  
2435 GGGACATGACCAACGAGATGTAATCATGGCATGACAGAGCATATGGCTGCCACCGC 2494  
DB 177 GGGACATGACCAACGAGATGTAATCATGGCATGACAGAGCATATGGCTGCCACCGC 236  
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DB 237 CCATGAGCTGGCCGAGCCCTGACACAACTCATGCTGGAGTGTGGCAGAGACCGCA 296  
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DB 297 ACCACGCTCCCAAGTTGGGCCAAATTGTCAACACGCTAGACAAAGATGATCCGCAATCCCA 356  
2615 ACAGCCTCAAGGCAATGGCGCCCTCTCTCTGAGATCAACCTGGCGCTGCTGGACCGCA 2674  
DB 357 ACAGCCTCAAGGCAATGGCGCCCTCTCTCTGAGATCAACCTGGCGCTGCTGGACCGCA 416  
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DB 417 CGATCCCGCA 426

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LOCUS BF766632  
DEFINITION BF766632  
ACCESSION BF766632.1 GI:12114532  
VERSION BF766632.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

# REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 440)

# AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

# TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

# JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
2020263

# COMMENT

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Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=IL2&t2=IL2-CS0048-  
221100-249-E10&t3=2000-11-22&t4=1)  
Seq primer: puc 18 forward  
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Location/Qualifiers

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/note="Organ: colon\_est; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT  
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ORIGIN

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DB 440 GAGAAAGTCCACATCATCGCTCTCGGCGCGCTGCGCTCTCTCATTTGCTGTG 381  
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DB 380 GTTGTCAATCGCCATCGTGTATCAACAGAGGGGTTTGAAGCTGCTGACTCGAGTACAG 321  
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1747 CATTTCACCTGACGAGACCCCAAGAGCAAGTGGGAGTTTGCAGAAATTTGACATC 1806  
DB 260 CATTTCACCTGACGAGACCCCAAGAGCAAGTGGGAGTTTGCAGAAATTTGACATC 201  
1807 TCCGTGTCAAAATTTGACAGAGTATCGACACAGGAGTTTGGCGAGTCTGCAGTGGC 1866  
DB 200 TCCGTGTCAAAATTTGACAGAGTATCGACACAGGAGTTTGGCGAGTCTGCAGTGGC 141  
1867 CACCTGAAGCTGCCAGCAGAGAGAGATCTTTGTGGCCATCAAGAGCTCAAGTGGGGC 1976  
DB 140 CACCTGAAGCTGCCAGCAGAGAGAGATCTTTGTGGCCATCAAGAGCTCAAGTGGGGC 81

Wed Jul 11 10:25:34 2001

us-09-378-759-10.011.rst

Page 12

OY 1927 TACACGAGAGCA 1940  
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Db 80 TACACGAGAGCA 67

Search completed: July 10, 2001, 20:11:58  
Job time: 5870 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 16:01:53 ; Search time 2160.18 Seconds  
(without alignments)  
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Title: US-09-378-759-10  
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Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2          | 657.4 | 22.2        | 2522   | 192   | AK017630    |
| 3          | 639.6 | 21.6        | 915    | 153   | BG425170    |
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| 17         | 480.2 | 16.2        | 552    | 31    | AV607557    |
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| 19         | 464.4 | 15.7        | 507    | 148   | BF441135    |
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| 21         | 442.2 | 14.9        | 932    | 141   | BE906826    |
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| 31         | 408.2 | 13.8        | 951    | 165   | BE272154    |
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| 41         | 384   | 13.0        | 440    | 169   | BF766632    |
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| 45         | 375   | 12.7        | 526    | 166   | BF736600    |

## ALIGNMENTS

| RESULT     | 1  | 787 bp | MRNA | EST         |
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| LOCUS      | AU119907   |        |      | 19-OCT-2000 |
| DEFINITION | AU119907 HEMBA1 Homo sapiens cDNA clone HEMBA1006901 5', mRNA        |        |      |             |
| ACCESSION  | AU119907   |        |      |             |
| VERSION    | AU119907.1   |        |      |             |
| KEYWORDS   | EST.   |        |      |             |
| SOURCE     | human.   |        |      |             |
| ORGANISM   | Homo sapiens   |        |      |             |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |        |      |             |
| AUTHORS    | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.           |        |      |             |
|            | Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., |        |      |             |
|            | Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and |        |      |             |
|            | Isogai, T.   |        |      |             |
| TITLE      | HRI human cDNA project   |        |      |             |

## JOURNAL COMMENT

Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix  
Research Institute; cDNA library construction; Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

## FEATURES

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DB 61 AGGACCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 1820 TTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1879
DB 121 TTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 1880 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1939
DB 181 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 1940 AGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1999
DB 241 AGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 2000 TCCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2059
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QY 2060 AGAATGGCTCCCTGGACCTCTTTCGCGCAAAAGAGAGGAGGAGGAGGAGGAGGAGGAG 2119
DB 361 AGAATGGCTCCCTGGACCTCTTTCGCGCAAAAGAGAGGAGGAGGAGGAGGAGGAGGAG 420
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DB 421 TGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
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DB 481 TTCACCGTACCTGCTGCGCGCAACATCTCGTAAAGCAAGCAAGCAAGCAAGCAAGG 540
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DB 541 CGGACCTTGGGCTTCACAGCTTTTAGAGAGAGATACCTCAGACCCGACCTACACAGG 600
QY 2300 CCCTGGGCGGAAAGTTCCCATCCGCTGAGACAGCCCGGAGGAGGAGGAGGAGGAGGAG 2359
DB 601 CCCTGGGCGGAAAGATCCCATCCGCTGAGACAGCCCGGAGGAGGAGGAGGAGGAGGAGG 660
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| QY         | 2420  | GGGAGCGGCCCTACTGTGGAGCATGACCA--CCAGGAGTATATCAAT--CCCATGTGAGCAGGA   | 2477            |
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| DB         | 781   | CTATCGG  | 787             |
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| LOCUS      | AK017630  |  |                 |
| DEFINITION | AK017630  | 2522 bp mRNA   | HTC 08-FEB-2001 |
| ACCESSION  | AK017630  | Mus musculus 8 days embryo CDNA, RIKEN full-length enriched library, clone:5730439123, full insert sequence. |                 |
| VERSION    | AK017630.1  | GI:12856968  |                 |
| KEYWORDS   | CAP trapper.  |  |                 |
| SOURCE     | Mus musculus (strain: C57BL/6J) 8 days embryo CDNA to mRNA, clone: 5730439123.  |  |                 |
| ORGANISM   | Mus musculus  |  |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |  |                 |
| AUTHORS    | Carninci, P. and Hayashizaki, Y.  |  |                 |
| TITLE      | High-efficiency full-length cDNA cloning  |  |                 |
| JOURNAL    | Methods Enzymol. 303, 19-44 (1999)  |  |                 |
| REFERENCE  | 2 (sites)   |  |                 |
| AUTHORS    | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.   |  |                 |
| TITLE      | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  |  |                 |
| JOURNAL    | Genome Res. 10 (10), 1617-1630 (2000)   |  |                 |
| MEDLINE    | 20499374  |  |                 |
| REFERENCE  | 3 (sites)   |  |                 |
| AUTHORS    | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komu, H., Akiyama, Y., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y.  |  |                 |
| TITLE      | RIKEN integrated sequence analysis (RISA) system--384-format  |  |                 |
| JOURNAL    | Genome Res. 10 (11), 1757-1771 (2000)   |  |                 |
| MEDLINE    | 20530913  |  |                 |
| REFERENCE  | 4 (sites)   |  |                 |
| AUTHORS    | The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.  |  |                 |
| TITLE      | Functional annotation of a full-length mouse cDNA collection  |  |                 |
| JOURNAL    | Nature 409, 685-690 (2001)  |  |                 |
| MEDLINE    | 5 (bases 1 to 2522)   |  |                 |
| REFERENCE  | Daichi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, Y., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hatanaka, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiroaki, T., Hoti, F., Imotoh, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Komu, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numata, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, K., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, K., Teijima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. |  |                 |
| TITLE      | Direct Submission   |  |                 |
| JOURNAL    | Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp),   |  |                 |

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research at Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'] GAGACGAGAAGATCCAGAGCCTGTCTTTTGGTTTTTTTNV N 3'. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence, [5'] GAGCGAGAGTCCTGCAGTAATTAAATAAATTAATCCCCCCC 3'). cDNA was cleaved with BamHI and XhoI. Vector: a modified phluescript KS(+) after bulk excision from lambda FLX I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

### FEATURES

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| CDS                       | BASE COUNT 563 a 622 c 725 g 612 t  |
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| Oy                        | 121 ACGATCCGACGTAACAGGTGTGCAACGTGTTGAGTCAAGCAGAACAACTGGCTACGG 180   |
| Db                        | 308 ACTATCCGTACTCTACAGGTGTGCAATGCTTTGAGTCAAGCACGAACAACCTGGCTGCG 367   |
| Oy                        | 181 ACCAAGTTTATCCGGCGCGGTGGGGGCCACCGCATCCAGTGGAGATGAAGTTTGGGTG 240  |
| Db                        | 368 ACCAAATTCATCCGGCGCGCGCGCGCGCACCGCATCCAGTGGAGATGAAGTTCTTGGGTG 427  |
| Oy                        | 241 CGTACTGACAGACATCCCGACAGCGTGCTGGCTCCGCAAGAGAGACTTCACACTCTAT 300  |
| Db                        | 428 CGTACTGACAGACATTCCTCCAGCGTGGCGGGCTCTGTGCAAGAGACCTTCAAACCTCTAC 487   |
| Oy                        | 301 TACTATGAGCTGACTTTGACTCGGCCACACAGACCTTCCCAACTGATGAGAAATCCA 360   |
| Db                        | 488 TACTATGAGCTGATTTTGACTTAGCCACAAAACCTTCCCAACTGATGAGAAATCCG 547  |
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**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)



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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 939)
NIH-MGC http://mhc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c99bs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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/notes="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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 Best Local Similarity 95.1%; Pred. No. 2, 1e-133;  
 Matches 674; Conservative 0; Mismatches 29; Indels 6; Gaps 5;

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 588)
NIH-MGC http://mhc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c99bs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL  
MEDLINE  
20202663  
COMMENT

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2=IL0-ST0002-160  
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## FEATURES

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No. 196/716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
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Location/Qualifiers  
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1 (bases 1 to 693)  
HCGP http://www.ludwig.org.br/ORESTES.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-CT0040-  
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from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## FEATURES

source

1. 693  
/organism="Homo sapiens"  
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/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
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Matches 561; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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| Oy | 2225 | TGGTCTCAAGAGTGTGCGACTTTGGGCTCTACGCTTTTAGAGAGCATTAACCTCGAAC    | 228 |
| Db | 424  | TGGTCTCAAAAGTGTGCGACTTTGGGCTTTCCGATTCCTGGAGAGAACTCTTCGATC     | 483 |
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| Oy        | 2582 - TCACACGCTGAGACAGATGATCCGCAATCCACACAGCCTCAAGGCATGG 2632  |          |
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| LOCUS      | 970 bp mRNA  |
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| ACCESSION  | AL552477   |
| VERSION    | AL552477.1 GI:12891411   |
| KEYWORDS   | EST.   |
| SOURCE     | human.   |
| ORGANISM   | Homo sapiens<br>Eukaryota; Chordata; Vertebrata; Euteleostomi;                       |

| REFERENCE                                       |                  |
|---|------------------|
| AUTHORS   |                  |
| TITLE   |                  |
| 1   | (bases 1 to 970) |
| Li, W.B., Gruber, C., Jesse, J. and Polayes, D. |                  |
| Full-length cDNA libraries and normalization    |                  |



[illegible]

QY 2003 .

Db 75 GCCTGGAGGGGTGTCACCAACAGATGCCGTCATATCTCTACAGATTTCATGGAGA 134

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Db 195 GTGGGCAATGCTTCGGGGCATGCGACAGTGGCAATGCTTCGGGACATGACATGTT 254

Qy 2182 CACGGTGCAGTGGGTCGGGCAACATCTCTGCAACACACACCTGCTGCAAGGTGCG 2241

Db 235 CACCGAGACCTGGGTCGGGCAACATCTCTGCAACACACACCTGCTGCAAGGTGCT 314

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Db 315 GACTTGGGCTCTTCCCAATTCCTGGAGAGAGATCTTCCGATCCCACTCAGCAGTGC 374

Qy 2301 CCTGGGCGAAAGTTCCCATTCCTGTCAGACAGCCCGGAGACCATTCAGTCCGAAATT 2360

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 ACCESSION AM938783.1 GI:8114229  
 VERSION  
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 SOURCE  
 ORGANISM

human.  
 Homo sapiens  
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 1 (bases 1 to 517)  
 Dlas Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,M.Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,B., Balis,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=4t2-pm3-DT0064-260  
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 No. 196,716 - Ludwig Institute for Cancer Research)  
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| ORGANISM                  | Homo sapiens   |  |                           |
| REFERENCE                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  |  |                           |
| AUTHORS                   | 1 (bases 1 to 912)   |  |                           |
| TITLE                     | Li, W.B., Gruber, C., Jessee, J. and Polayes, D.   |  |                           |
| JOURNAL                   | Full-length cDNA libraries and normalization   |  |                           |
| COMMENT                   | Unpublished (2001)   |  |                           |
| CONTACT                   | Contact: Genoscope   |  |                           |
| GENOSCOPE                 | Genoscope - Centre National de Sequencage  |  |                           |
| BP                        | BP 191 91006 Evry cedex - France   |  |                           |
| Email:                    | secre@genoscope.cns.fr, Web : www.genoscope.cns.fr.  |  |                           |
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|                           | /tissue.type="Placenta"  |  |                           |
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| BASE COUNT                | 190 a 280 c 253 g 184 t  | 5 others   |                           |
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| Best Local Similarity     | 75.5%;   | Pred. No. 3.1e-109;  |                           |
| Matches 680; Conservative | 4;   | Mismatches 211;  | Indels 6; Gaps 5;         |
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| Db                        | 1  | TCATCATATGAGGCACTTGTGAGACCAATATCACTCCGCTTGAGAGGCTGTACCAAC        | 60                        |
| QY                        | 2026   | AGCACACTGTGATGATCATCATCGAGTTTCATGAGAAATGCTCCCTGACTCTTTTTC        | 2085                      |
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| Db                        | 121  | CGGCTAAACGACGACAGTTCACAGTTCATCCAGCTGAGTGGGATGATCTTCGCGGCAATCGC   | 180                       |
| QY                        | 2146   | GCTGGCATGAAGTACTCTGGACAGATGAACTATGTAATGTTCAACCGGACCTGGTCCCGCAAC  | 2205                      |
| Db                        | 181  | TCGGGCATGCGGTACTTGGCGAGATGAGTACGTCACACCGAGACTGGCTGCTCGCAAC       | 240                       |
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| Y                         | 2326   | TGACACAGCCCCGGAAGCCATCAGTACCGGAAAGTTTCACCTTGCGGACGATGATGTGGAGC   | 2385                      |

| Db         | Accession   | Source   | Organism | Reference | Authors       | Title | Journal | Comment |
|------------|---|--|----------|-----------|---------------|-------|---------|---------|
| Db         | 361   | 166AGCTGCCCCGGAGGCCATTTCCTTCCGGAGTTCACTTCGCCAGTATGCTGGAGT        | 420      |           |               |       |         |         |
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| Db         | 481   | AATCAAGAGATGTATCAATGCCATTAGACAGAGCTACCGGCTKCYCCCCCCCCAGACTGT     | 540      |           |               |       |         |         |
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| Db         | 541   | TCCACTTCCTTCACACAGCTCATGCTTGGACTGTGTGGACAGAAAGGAGCCGCAATGCCCGGCC | 600      |           |               |       |         |         |
| QY         | 2566  | AGGTTGGGCAATTTGTCAACACAGCTAGACACAGATGATCCGCAATCCCAAC-AGCTCTCA    | 2624     |           |               |       |         |         |
| Db         | 601   | CGCTTCCCCACAGTGTGTGAGCGCCCTGGACAAAGATGATCCGGAACCCGCCBAGCTCA      | 660      |           |               |       |         |         |
| QY         | 2625  | AGCCATGGAGGCCCTCTCTCTCTGCGATCAACCTGCGCTGCTGGACCGCAGATCCCGA       | 2684     |           |               |       |         |         |
| Db         | 661   | AATCGTGGCCCGGAGAAATGGCGGGGCCCTCAACCCCTCTCTGGACC-AGCGGCACTCA      | 719      |           |               |       |         |         |
| QY         | 2685  | CTACACACAGCTTTACACGGTGGAGAGAGTGGCTGGAGGCCATCAAGATGGGGAGTACAA     | 2744     |           |               |       |         |         |
| Db         | 720   | CTACTCAGCTTTGGCTCTGTGTGGGAGATGGCTTGGGSSCATCAAAATGGGAGATACGA      | 779      |           |               |       |         |         |
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| ORGANISM   | Homo sapiens  |  |          |           |               |       |         |         |
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| AUTHORS    | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |  |          |           |               |       |         |         |
| TITLE      | 1 (bases 1 to 523)  |  |          |           |               |       |         |         |
| JOURNAL    | NIH-MGC http://mgs.nci.nih.gov/                                   |  |          |           |               |       |         |         |
| COMMENT    | National Institutes of Health, Mammalian Gene Collection (MGC)    |  |          |           |               |       |         |         |
|            | Unpublished (1999)  |  |          |           |               |       |         |         |
|            | Contact: Robert Strausberg, Ph.D.                                 |  |          |           |               |       |         |         |
|            | Email: cgapds-1@mail.nih.gov                                      |  |          |           |               |       |         |         |
|            | Tissue Procurement: ATCC  |  |          |           |               |       |         |         |
|            | CDNA Library Preparation: Ling Hong/Rubin Laboratory              |  |          |           |               |       |         |         |
|            | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)          |  |          |           |               |       |         |         |
|            | DNA sequencing by: Incyte Genomics, Inc.                          |  |          |           |               |       |         |         |
|            | Clone distribution: MGC clone distribution information can be     |  |          |           |               |       |         |         |
|            | found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov     |  |          |           |               |       |         |         |
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adaptor: GGACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."  
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Db 361 AAGGCGCTTACTGACAGGAGCCCTTCTGCGCTGAGTGTGCGCTGTAATCAGCAGC 420  
QY 1252 AAGCAGGAGCTCATCGGAGTGTTCATTCATGATGATGAGGCGGACCGTGGACAGC 1311  
Db 421 AAGCAGGAGCTCATCGGAGTGTTCATTCATGATGATGAGGCGGACCGTGGACAGC 480  
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 758)  
AUTHORS HGCP <http://www.ludwig.org.br/ORESTES>.  
TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/genhtml2.pl?IL0-CT0002-050899-058-c02&L3-1999-08-05&L4-1>)  
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Location/Qualifiers

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into the pUC 18 vector. Reverse transcription of tissue  
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Page 14

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GenCore version 4.5  
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Searched: 392237 seqs, 148486726 residues

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4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                                |
|------------|-------|-------------|--------|-------|--|
| 1          | 30    | 1.0         | 3836   | 5     | US-09-560-875A-7981<br>Sequence 7981, App  |
| 2          | 23    | 0.8         | 399    | 5     | US-09-872-850-298<br>Sequence 298, App     |
| 3          | 23    | 0.8         | 504    | 5     | US-09-872-850-301<br>Sequence 301, App     |
| 4          | 21    | 0.8         | 2451   | 5     | US-09-771-161A-4<br>Sequence 4, Appl       |
| 5          | 21    | 0.7         | 4016   | 5     | US-09-560-875A-6907<br>Sequence 6907, App  |
| 6          | 19    | 0.5         | 382    | 5     | US-09-693-692-967<br>Sequence 316, App     |
| 7          | 19    | 0.5         | 2083   | 1     | PCR-US01-10485A-316<br>Sequence 7710, App  |
| 8          | 19    | 0.5         | 5374   | 5     | US-09-560-875A-7710<br>Sequence 7710, App  |
| 9          | 19    | 0.5         | 16350  | 5     | US-09-793-706A-3<br>Sequence 2326, App     |
| 10         | 18    | 0.6         | 207    | 4     | US-08-221-623D-2326<br>Sequence 12431, A   |
| 11         | 18    | 0.6         | 327    | 5     | US-09-371-146A-12431<br>Sequence 760, App  |
| 12         | 18    | 0.6         | 487    | 5     | US-09-649-165A-760<br>Sequence 253158, App |
| 13         | 18    | 0.6         | 525    | 5     | US-09-371-146A-253158<br>Sequence 5, Appl  |
| 14         | 17    | 0.6         | 109    | 5     | US-09-237-183A-5<br>Sequence 133, App      |
| 15         | 17    | 0.6         | 128    | 5     | US-09-237-183A-133<br>Sequence 5, Appl     |
| 16         | 17    | 0.6         | 149    | 5     | US-09-872-850-5<br>Sequence 134, App       |
| 17         | 17    | 0.6         | 150    | 5     | US-09-337-183A-134<br>Sequence 69843, A    |
| 18         | 17    | 0.6         | 150    | 5     | US-09-371-146A-69843<br>Sequence 127, App  |
| 19         | 17    | 0.6         | 171    | 5     | US-09-237-183A-127<br>Sequence 66812, A    |
| 20         | 17    | 0.6         | 171    | 5     | US-09-371-146A-66812<br>Sequence 82, Appl  |
| 21         | 17    | 0.6         | 182    | 5     | US-09-237-183A-82<br>Sequence 42876, A     |
| 22         | 17    | 0.6         | 182    | 5     | US-09-371-146A-42876<br>Sequence 115, App  |
| 23         | 17    | 0.6         | 203    | 5     | US-09-237-183A-115<br>Sequence 54399, A    |
| 24         | 17    | 0.6         | 203    | 5     | US-09-371-146A-54399<br>Sequence 108, App  |
| 25         | 17    | 0.6         | 204    | 5     | US-09-237-183A-108<br>Sequence 2129, App   |
| 26         | 17    | 0.6         | 204    | 5     | US-09-371-146A-2129<br>Sequence 117, App   |
| 27         | 17    | 0.6         | 209    | 5     | US-09-237-183A-117<br>Sequence 117, App    |

|      |    |     |     |   |   |
|------|----|-----|-----|---|---|
| C 28 | 17 | 0.6 | 212 | 5 | US-09-237-183A-130<br>Sequence 130, App   |
| C 29 | 17 | 0.6 | 212 | 5 | US-09-371-146A-42667<br>Sequence 42667, A |
| C 30 | 17 | 0.6 | 216 | 5 | US-09-237-183A-106<br>Sequence 106, App   |
| C 31 | 17 | 0.6 | 216 | 5 | US-09-237-183A-118<br>Sequence 118, App   |
| C 32 | 17 | 0.6 | 216 | 5 | US-09-371-146A-55273<br>Sequence 55273, A |
| C 33 | 17 | 0.6 | 216 | 5 | US-09-371-146A-62741<br>Sequence 62741, A |
| C 34 | 17 | 0.6 | 216 | 5 | US-09-237-183A-121<br>Sequence 121, App   |
| C 35 | 17 | 0.6 | 238 | 5 | US-09-371-146A-18923<br>Sequence 18923, A |
| C 36 | 17 | 0.6 | 240 | 5 | US-09-237-183A-129<br>Sequence 129, App   |
| C 37 | 17 | 0.6 | 240 | 5 | US-09-371-146A-19740<br>Sequence 19740, A |
| C 38 | 17 | 0.6 | 243 | 5 | US-09-371-146A-70051<br>Sequence 70051, A |
| C 39 | 17 | 0.6 | 246 | 5 | US-09-237-183A-128<br>Sequence 128, App   |
| C 40 | 17 | 0.6 | 246 | 5 | US-09-371-146A-23844<br>Sequence 116, App |
| C 41 | 17 | 0.6 | 255 | 5 | US-09-237-183A-116<br>Sequence 4552, App  |
| C 42 | 17 | 0.6 | 255 | 5 | US-09-371-146A-4552<br>Sequence 112, App  |
| C 43 | 17 | 0.6 | 259 | 5 | US-09-237-183A-112<br>Sequence 22925, A   |
| C 44 | 17 | 0.6 | 259 | 5 | US-09-371-146A-22925<br>Sequence 196, App |
| C 45 | 17 | 0.6 | 260 | 5 | US-09-237-183A-156<br>Sequence 156, App   |

#### ALIGNMENTS

```

RESULT 1
US-09-560-875A-7981
; Sequence 7981, Application US/09560875A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Slinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radjic T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 787
; CURRENT APPLICATION NUMBER: US/09/560,875A
; CURRENT FILING DATE: 2000-04-27
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10410
; SOFTWARE: PLCT_genes Version 1.02
; SEQ ID NO 7981
; LENGTH: 3836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3836)
; OTHER INFORMATION: n = a,t,c or g
; NAME/KEY: misc_feature
; LOCATION: (28)...(3024)
; OTHER INFORMATION: similar to g1406868 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3f00, default parameters
US-09-560-875A-7981

Query Match 1.0%: Score 30; DB 5; Length 3836;
Best Local Similarity 100.0%: Pred. No. 1.2e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 GGGTGGAGAGGTGAGTGCCTACGATGAG 111
DB 208 ggggtgggaagagtgatgagtcacgatgag 237

RESULT 2
US-09-872-850-298
; Sequence 298, Application US/09872850
; GENERAL INFORMATION:
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Escobedo, Jaime
; APPLICANT: Reinhard, Christoph
; APPLICANT: Randazzo, Filippo
; APPLICANT: Lamson, George

```

APPLICANT: Garcia, Pablo  
APPLICANT: Kaufmann, Joerg  
APPLICANT: Kennedy, Giulia  
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
IN CANCEROUS COLON CELLS  
FILE REFERENCE: 15805.002  
CURRENT APPLICATION NUMBER: US/09/872.850  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 60/208,871  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 298  
LENGTH: 399  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(399)  
OTHER INFORMATION: n = A,T,C or G  
US-09-872-850-298

Query Match 0.8%; Score 23; DB 5; Length 399;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 GTCACAGCACTGCTGCGAA 2234  
|||||  
Db 54 gtcaacagcaacctgctcgcaa 76

RESULT 3  
US-09-872-850-301  
Sequence 301, Application US/09872850  
GENERAL INFORMATION:  
APPLICANT: Sudduth-Klinger, Julie  
APPLICANT: Escobedo, Jaime  
APPLICANT: Reinhard, Christoph  
APPLICANT: Randazzo, Filippo  
APPLICANT: Lamson, George  
APPLICANT: Garcia, Pablo  
APPLICANT: Kaufmann, Joerg  
APPLICANT: Kennedy, Giulia  
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
IN CANCEROUS COLON CELLS  
FILE REFERENCE: 15805.002  
CURRENT APPLICATION NUMBER: US/09/872.850  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 60/208,871  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 301  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(504)  
OTHER INFORMATION: n = A,T,C or G  
US-09-872-850-301

Query Match 0.8%; Score 23; DB 5; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 GTCACAGCACTGCTGCGAA 2234  
|||||  
Db 45 gtcaacagcaacctgctcgcaa 67

RESULT 4  
US-09-771-161A-4  
Sequence 4, Application US/09771161A  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771.161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 2451  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: -  
LOCATION: (1)...(2451)  
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-4

Query Match 0.8%; Score 23; DB 5; Length 2451;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2326 TGGACAGCCCCGGAGACCATCCA 2348  
|||||  
Db 1636 tggacagccccggagaccatcca 1658

RESULT 5  
US-09-560-875A-6907  
Sequence 6907, Application US/09560875A  
GENERAL INFORMATION:  
APPLICANT: Tang, Yuanhua T.  
APPLICANT: Tillinghast, John  
APPLICANT: Sinku, Ankura  
APPLICANT: Liu, Chenohua  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: Novel Contigs Obtained  
From Various Libraries  
FILE REFERENCE: 787  
CURRENT APPLICATION NUMBER: US/09/560,875A  
CURRENT FILING DATE: 2000-04-27  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 10410  
SOFTWARE: PL\_CT\_genes Version 1.02  
SEQ ID NO 6907  
LENGTH: 4016  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (712)...(3850)  
OTHER INFORMATION: similar to g1177466 in the genepept database release 114,  
OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
US-09-560-875A-6907

Query Match 0.7%; Score 21; DB 5; Length 4016;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GAGTGGCTGTGCCCATCGG 714  
|||||  
Db 1552 gagtggctgtgtcccatcggg 1572





RESULT 10  
US-08-221-623D-2326  
; Sequence 2326, Application US/08221623D  
; GENERAL INFORMATION:  
; APPLICANT: Adams, et al.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products  
; FILE REFERENCE: PG-10  
; CURRENT APPLICATION NUMBER: US/08/221,623D  
; CURRENT FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 3321  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2326  
; LENGTH: 207  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (63)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (140)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (175)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-08-221-623D-2326

Query Match 0.6%; Score 18; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1143 CAGTGACCTGCTGCCCA 1160  
|||||

Db 1 cagtgacctgctgcccga 18

RESULT 11  
US-09-371-146A-12431/c  
; Sequence 12431, Application US/09371146A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: ANNOTATED PLANT GENES  
; FILE REFERENCE: 38-21(15097)C  
; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 12431  
; LENGTH: 327  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-371-146A-12431

Query Match 0.6%; Score 18; DB 5; Length 327;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 AGGAGACCTTCAACCTCT 298  
|||||

Db 59 AGGAGACCTTCAACCTCT 42

RESULT 12  
US-09-649-165A-760  
; Sequence 760, Application US/09649165A  
; GENERAL INFORMATION:  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Doyle, Martin  
; APPLICANT: Momiyama, Monika

APPLICANT: Mang, Xinhao  
; TITLE OF INVENTION: DETECTING EXPRESSION OF ARABIDOPSIS THALIANA GENES  
; FILE REFERENCE: PA-0019 US  
; CURRENT APPLICATION NUMBER: US/09/649,165A  
; CURRENT FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/150,517  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 7753  
; SOFTWARE: PERL Program  
; SEQ ID NO 760  
; LENGTH: 487  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: lacyte ID No: 701495952  
US-09-649-165A-760

Query Match 0.6%; Score 18; DB 5; Length 487;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGAACCTGTCGCGG 597  
|||||

Db 393 caggaacctgctcgcg 410

RESULT 13  
US-09-371-146A-253158/c  
; Sequence 253158, Application US/09371146A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: ANNOTATED PLANT GENES  
; FILE REFERENCE: 38-21(15097)C  
; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 253158  
; LENGTH: 525  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-371-146A-253158

Query Match 0.6%; Score 18; DB 5; Length 525;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1031 ACAACATCATCTGCAGA 1048  
|||||

Db 230 ACAACATCATCTGCAGA 213

RESULT 14  
US-09-237-183A-5/c  
; Sequence 5, Application US/09237183A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The  
; FILE REFERENCE: 38-21(15089)B  
; CURRENT APPLICATION NUMBER: US/09/237,183A  
; CURRENT FILING DATE: 1999-01-26  
; PRIOR APPLICATION NUMBER: US 60/067,000  
; PRIOR FILING DATE: 1997-11-24  
; NUMBER OF SEQ ID NOS: 2814  
; SEQ ID NO 5

LENGTH: 109  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-237-183A-5

Query Match 0.6%; Score 17; DB 5; Length 109;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 GGTCCGAGACTTCGAC 460  
|||||  
DB 74 GGTCCGAGACTTCGAC 58

RESULT 15  
US-09-237-183A-133/C  
Sequence 133, Application US/09237183A  
GENERAL INFORMATION:  
APPLICANT: Fisher, Dane K.  
APPLICANT: Liu, Jingdong  
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The  
FILE REFERENCE: 38-21(15089)B  
CURRENT APPLICATION NUMBER: US/09/237,183A  
PRIOR APPLICATION NUMBER: US 60/067,000  
PRIOR FILING DATE: 1997-11-24  
NUMBER OF SEQ ID NOS: 2814  
SEQ ID NO 133  
LENGTH: 128  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-237-183A-133

Query Match 0.6%; Score 17; DB 5; Length 128;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 GGTCCGAGACTTCGAC 460  
|||||  
DB 55 GGTCCGAGACTTCGAC 39

Search completed: July 10, 2001, 22:21:38  
Job time: 7775 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 15:07:58 ; Search time 3870.77 Seconds

(without alignments)  
11836.269 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CTGCTGCCCGCCGTGAGAGA.....CCAGCCCCCGCCCTCTGC 2962

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rtd:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rtd:*
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36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*

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44: em_ov:*
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47: em_pl:*
48: em_ro:*
49: em_sts:*
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51: em_un:*
52: em_v1:*
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57: gb_un:*
58: gb_v11:*
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93: gb_v46:*
94: gb_v47:*
95: gb_v48:*
96: gb_v49:*
97: gb_v50:*
98: em_ba3:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID       | Description        |
|------------|--------|-------------|--------|-------------|--------------------|
| 1          | 2962   | 100.0       | 2962   | 9 AR084933  | AR084933 Sequence  |
| 2          | 2962   | 100.0       | 2962   | 9 AR084949  | AR084949 Sequence  |
| 3          | 2961.6 | 100.0       | 2962   | 97 HUMRPTKA | L36643 Homo sapien |
| 4          | 2923.4 | 98.7        | 3768   | 9 AX034853  | AX034853 Sequence  |
| 5          | 2923.4 | 98.7        | 3768   | 97 HUMDRRT  | L41939 Homo sapien |
| 6          | 2897.2 | 97.8        | 3151   | 97 HUMERRA  | D31661 Human mRNA  |
| 7          | 2884   | 97.4        | 3949   | 9 AX034855  | AX034855 Sequence  |
| 8          | 2884   | 97.4        | 3949   | 88 AF025304 | AF025304 Homo sapi |



QY 1201 ACTGACCAAGCCCTCTGCGCTCACTGCGCTGTGAAACATACACCACAGGCA 1260  
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 DB 1201 ACTGACCAAGCCCTCTGCGCTCACTGCGCTGTGAAACATACACCACAGGCA 1260  
 QY 1261 GCTCCATCGGAGAGTGTGATCATCATGAGTGAGCGGACCGGAGACAGATTAACCTG 1320  
 |||||||  
 DB 1261 GCTCCATCGGAGAGTGTGATCATCATGAGTGAGCGGACCGGAGACAGATTAACCTG 1320  
 QY 1321 TCGGTGTCCAGCGGACGACCAATGAGCGTGTGATCTGAGCTATGAGCTGCACTAT 1380  
 |||||||  
 DB 1321 TCGGTGTCCAGCGGACGACCAATGAGCGTGTGATCTGAGCTATGAGCTGCACTAT 1380  
 QY 1381 GAGAGGAGCTCACTGAGTACACAGCCACAGCCATAAAAAGCCCAACACAGGTCACG 1440  
 |||||||  
 DB 1381 GAGAGGAGCTCACTGAGTACACAGCCACAGCCATAAAAAGCCCAACACAGGTCACG 1440  
 QY 1441 GGCTCAAAAGCGGCGGCTATGTCTTCAGAGTGGGCGGACGACCTGTGGACGCTAC 1500  
 |||||||  
 DB 1441 GGCTCAAAAGCGGCGGCTATGTCTTCAGAGTGGGCGGACGACCTGTGGACGCTAC 1500  
 QY 1501 GGGGCTACAGCGGACGAGTACTTCCAGACATGACAGAGCGAGTACAGACAGC 1560  
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 DB 1501 GGGGCTACAGCGGACGAGTACTTCCAGACATGACAGAGCGAGTACAGACAGC 1560  
 QY 1561 ATCCAGGAGAGTGGCCACTCATCATCGGCTCTCGGCGGCTGGCTGTGCTCTCAT 1620  
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 DB 1561 ATCCAGGAGAGTGGCCACTCATCATCGGCTCTCGGCGGCTGGCTGTGCTCTCAT 1620  
 QY 1621 GCTGTGTGTGTCATCGGCTATGTGTAAACAGAGGCGGCTTGGAGCTGCTGAG 1680  
 |||||||  
 DB 1621 GCTGTGTGTGTCATCGGCTATGTGTAAACAGAGGCGGCTTGGAGCTGCTGAG 1680  
 QY 1681 TACACGGACAGCTGCAACACTACACAGTGGCCACATTAACCCAGGATGAAGTCTAC 1740  
 |||||||  
 DB 1681 TACACGGACAGCTGCAACACTACACAGTGGCCACATTAACCCAGGATGAAGTCTAC 1740  
 QY 1741 ATCCAGGAGAGTGGCCACTCATCATCGGCTCTCGGCGGCTGGCTGTGCTCTCAT 1800  
 |||||||  
 DB 1741 ATCCAGGAGAGTGGCCACTCATCATCGGCTCTCGGCGGCTGGCTGTGCTCTCAT 1800  
 QY 1801 GACATCTCTGTGTCAAAATTTGACAGAGTGTGAGGAGCGGAGTTTGGGAGGCTGCG 1860  
 |||||||  
 DB 1801 GACATCTCTGTGTCAAAATTTGACAGAGTGTGAGGAGCGGAGTTTGGGAGGCTGCG 1860  
 QY 1861 AGTGCCACCTGTAAGCTGCGCAGGCAAGAGAGATCTTGTGGCCATCAACAGCTCAAG 1920  
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 DB 1861 AGTGCCACCTGTAAGCTGCGCAGGCAAGAGAGATCTTGTGGCCATCAACAGCTCAAG 1920  
 QY 1921 TCGGGCTACAGGAGAGCAGCGCGGAGCTTCTGAGCGAAGCCTCCATCATGGGCGAG 1980  
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 DB 1921 TCGGGCTACAGGAGAGCAGCGCGGAGCTTCTGAGCGAAGCCTCCATCATGGGCGAG 1980  
 QY 1981 TTGCAACCATCCCAACGTCATCATCGAGGAGTGTGTCGACCAAGAGCAGCTGTGATG 2040  
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 DB 1981 TTGCAACCATCCCAACGTCATCATCGAGGAGTGTGTCGACCAAGAGCAGCTGTGATG 2040  
 QY 2041 ATCATACACGAGTTCATGAGAGATGGCTCCTGAGACTCTTCTCCGCGCAAAAGAGTGGG 2100  
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 DB 2041 ATCATACACGAGTTCATGAGAGATGGCTCCTGAGACTCTTCTCCGCGCAAAAGAGTGGG 2100  
 QY 2101 CAGTTTACAGTTCATGAGAGTGGGCTGTGCTGGGCGCATCGCAGCTGTGATGATG 2160  
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 DB 2101 CAGTTTACAGTTCATGAGAGTGGGCTGTGCTGGGCGCATCGCAGCTGTGATGATG 2160  
 QY 2161 CTGGCAGACATGAATATGTTTACAGCTGAGCTGGCTGCCCGCAACATCTCTGTAACAGC 2220  
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 DB 2161 CTGGCAGACATGAATATGTTTACAGCTGAGCTGGCTGCCCGCAACATCTCTGTAACAGC 2220  
 QY 2221 AACCTGCTCTGCAAGAGTGTGGAGCTTGGGCTCTACAGCTTCTTGAAGAGATACCTCA 2280  
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 DB 2221 AACCTGCTCTGCAAGAGTGTGGAGCTTGGGCTCTACAGCTTCTTGAAGAGATACCTCA 2280

QY 2281 GACCCACCTACACACAGTGGCCCTGGGGAAGTTTCCCAATCCGCTGGACAGCCCGGAA 2340  
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 DB 2281 GACCCACCTACACACAGTGGCCCTGGGGAAGTTTCCCAATCCGCTGGACAGCCCGGAA 2340  
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 DB 2341 GGCATCCAGTACCGGAAGTTCACCTCGGCGCAGTATGTGTGAGCTACAGGATTTGTCATG 2400  
 QY 2401 TGGGAGGTGATGTCTTATGGGAGCGGCGCTTACGTGGGACATGACCAACAGAGTGAATC 2460  
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 DB 2401 TGGGAGGTGATGTCTTATGGGAGCGGCGCTTACGTGGGACATGACCAACAGAGTGAATC 2460  
 QY 2461 AATGCCATTGAGCAGAGATATCGGCTGCCACCGCCCATGAGACTGCCGAGGCGCTGAC 2520  
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 DB 2461 AATGCCATTGAGCAGAGATATCGGCTGCCACCGCCCATGAGACTGCCGAGGCGCTGAC 2520  
 QY 2521 CAACCTATGCTGAGCTGTGGCAGAGAGACCGCAACACCGGCGCAAGTTGGGCAAAAT 2580  
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 DB 2521 CAACCTATGCTGAGCTGTGGCAGAGAGACCGCAACACCGGCGCAAGTTGGGCAAAAT 2580  
 QY 2581 GTCAACACGCTAGACAGAGATATCGGCTGCCACCGCCCATGAGACTGCCGAGGCGCTGAC 2640  
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 QY 2641 TCTCTGTGCTACAACTGCGCTGCTGAGACCGCAGAGATCCCGGACTACAGCTTTTAA 2700  
 |||||||  
 DB 2641 TCTCTGTGCTACAACTGCGCTGCTGAGACCGCAGAGATCCCGGACTACAGCTTTTAA 2700  
 QY 2701 ACGGTGGAGAGTGGGCTGGGAGGCGCATCAAGATGGGCGAGTCAAGAGAGCTTGGCCANT 2760  
 |||||||  
 DB 2701 ACGGTGGAGAGTGGGCTGGGAGGCGCATCAAGATGGGCGAGTCAAGAGAGCTTGGCCANT 2760  
 QY 2761 GCCGCTTACACCTCTTGTGAGCTGTGTCTCAGATGATGATGAGAGATTTCTCGGGTT 2820  
 |||||||  
 DB 2761 GCCGCTTACACCTCTTGTGAGCTGTGTCTCAGATGATGATGAGAGATTTCTCGGGTT 2820  
 QY 2821 GGGGCTACTTTGGCTGGCGCAGCAAAAAAATCTGACAGATATTCAGGATGAGGCGG 2880  
 |||||||  
 DB 2821 GGGGCTACTTTGGCTGGCGCAGCAAAAAAATCTGACAGATATTCAGGATGAGGCGG 2880  
 QY 2881 CAGATGAACAGATTCAGTGTGTGAGGTTGACATTCACCTGCTGAGCTCACCTTTC 2940  
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 DB 2881 CAGATGAACAGATTCAGTGTGTGAGGTTGACATTCACCTGCTGAGCTCACCTTTC 2940  
 QY 2941 CTCGAAGCCCGCCCTCTCTGC 2962  
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 DB 2941 CTCGAAGCCCGCCCTCTCTGC 2962  
 RESULT 2  
 AR084949 2962 bp DNA PAT 01-SEP-2000  
 LOCUS AR084949 Sequence 10 from patent US 5981246.  
 DEFINITION AR084949  
 ACCESSION AR084949.1 GI:10011720  
 VERSION AR084949.1  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2962)  
 AUTHORS Fox, G.M., Welcher, A.A. and Jing, S.  
 TITLE Nucleic acids encoding Eph-like receptor protein tyrosine kinases  
 JOURNAL Patent: US 5981246-A 10 09-NOV-1999;  
 FEATURES Location/Qualifiers  
 source 1..2962  
 BASE COUNT 654 a 914 c 827 g 567 t  
 ORIGIN  
 Query Match 100.0%; Score 2962; DB 9; Length 2962;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1 CTGTCGCCCGCTGGAAGAAAGCTAATGAGACTCCACTACAGGACTGCTGAGCTGGC 60  
DB 1 CTGTCGCCCGCTGGAAGAAAGCTAATGAGACTCCACTACAGGACTGCTGAGCTGGC 60  
OY 61 TGGATGATGATCTCTCCATCAGGATGGGAAGAGGTGATGATGATGATGATGATGATGAT 120  
DB 61 TGGATGATGATCTCTCCATCAGGATGGGAAGAGGTGATGATGATGATGATGATGATGAT 120  
OY 121 ACCATCCGACGATACCAAGGTGTGCAACGTTTGTGATGCAAGCCAGAACTGGCTACGG 180  
DB 121 ACCATCCGACGATACCAAGGTGTGCAACGTTTGTGATGCAAGCCAGAACTGGCTACGG 180  
OY 181 ACCAAGTTATCCGGGCGCGTGGGGGCCACCGCATCCACGTGGAGATGAAGTTTGGTG 240  
DB 181 ACCAAGTTATCCGGGCGCGTGGGGGCCACCGCATCCACGTGGAGATGAAGTTTGGTG 240  
OY 241 CGTACTGACGACGATCCCGAGCGTCTGGCTCTGCAAGGAGACCTTCAACCTCTAT 300  
DB 241 CGTACTGACGACGATCCCGAGCGTCTGGCTCTGCAAGGAGACCTTCAACCTCTAT 300  
OY 301 TACTATGAGGCTGACTTGTGATCTGGGCGACCAAGACCTTCCCAACTGGATGGAAATCCA 360  
DB 301 TACTATGAGGCTGACTTGTGATCTGGGCGACCAAGACCTTCCCAACTGGATGGAAATCCA 360  
OY 361 TGGGTGAGGTGATACCATTTGACGCGACGAGAGCTTCTCCAGGTGAGCTGGGTGGC 420  
DB 361 TGGGTGAGGTGATACCATTTGACGCGACGAGAGCTTCTCCAGGTGAGCTGGGTGGC 420  
OY 421 CGGCTCATGAAATCAACACCGAGGTGCGAGCTTGGAGCTGTGTCGCGACGCGCTTC 480  
DB 421 CGGCTCATGAAATCAACACCGAGGTGCGAGCTTGGAGCTGTGTCGCGACGCGCTTC 480  
OY 481 TACTGCGCTCTCAGAGCTATGGGCGCTGCATGCTCTCATTCGCCGCTGCTTCTTAC 540  
DB 481 TACTGCGCTCTCAGAGCTATGGGCGCTGCATGCTCTCATTCGCCGCTGCTTCTTAC 540  
OY 541 CGCAAGTGCCTCCGACATCATGCAAAATGGGCGCATCTTCCAGGAAACCTGTGGGGGCT 600  
DB 541 CGCAAGTGCCTCCGACATCATGCAAAATGGGCGCATCTTCCAGGAAACCTGTGGGGGCT 600  
OY 601 GAGAGACATGCTGTGTGCTGCCCGGGGAGCTGCATGCGCAATGGGGAAGAGTGGAT 660  
DB 601 GAGAGACATGCTGTGTGCTGCCCGGGGAGCTGCATGCGCAATGGGGAAGAGTGGAT 660  
OY 661 GTACCATCAAGCTCTACTGTATACGGGAGGAGGAGTGGTGGTGGCCATCGGGCGCTGC 720  
DB 661 GTACCATCAAGCTCTACTGTATACGGGAGGAGGAGTGGTGGTGGCCATCGGGCGCTGC 720  
OY 721 ATGTGCAAGGAGGCTTGAAGGCGCTTGAAGATGGCACCTCTGCGGAGGTTTGTTCATCT 780  
DB 721 ATGTGCAAGGAGGCTTGAAGGCGCTTGAAGATGGCACCTCTGCGGAGGTTTGTTCATCT 780  
OY 781 GGGACTTTTCAAGGCCAACCAAGGGGATGAGGCTGTATCCCATGCTCCATCAACAGCGG 840  
DB 781 GGGACTTTTCAAGGCCAACCAAGGGGATGAGGCTGTATCCCATGCTCCATCAACAGCGG 840  
OY 841 ACCACTTCTGAAGGGGCGAACCACTGTGTGCGCAATGGCTACTACAGAGACCTG 900  
DB 841 ACCACTTCTGAAGGGGCGAACCACTGTGTGCGCAATGGCTACTACAGAGACCTG 900  
OY 901 GACCCCTGAGACATGCTTGAAGGCGCAACCACTGCGGCGCCAGGCTGTGATTTCCAGT 960  
DB 901 GACCCCTGAGACATGCTTGAAGGCGCAACCACTGCGGCGCCAGGCTGTGATTTCCAGT 960  
OY 961 GTCAATGAGACCTCTCTATGCTGAGTGAAGGACCTCCCGCGACTCCGAGGCGAGAG 1020  
DB 961 GTCAATGAGACCTCTCTATGCTGAGTGAAGGACCTCCCGCGACTCCGAGGCGAGAG 1020  
OY 1021 GACCTGCTACAACTATCTGCAAGAGCTGTGGGCGGGGGGCTGCTGACACCGC 1080  
DB 1021 GACCTGCTACAACTATCTGCAAGAGCTGTGGGCGGGGGGCTGCTGACACCGC 1080

OY 1081 TGGGGGACATGTACAGTACGACCAAGCAGGTAGGCTGAGCCGACGACCATTTAC 1140  
DB 1081 TGGGGGACATGTACAGTACGACCAAGCAGGTAGGCTGAGCCGACGACCATTTAC 1140  
OY 1141 ATCAGTACCTGCTGAGCCACACCACTACACCTTGAAGTCCAGGCTGTGAAGGGCTT 1200  
DB 1141 ATCAGTACCTGCTGAGCCACACCACTACACCTTGAAGTCCAGGCTGTGAAGGGCTT 1200  
OY 1201 ACTGACCAAGCCCTTCTGCGCTCAAGTTCGCTGTGAACATCACACCAACGAGCA 1260  
DB 1201 ACTGACCAAGCCCTTCTGCGCTCAAGTTCGCTGTGAACATCACACCAACGAGCA 1260  
OY 1261 GCTTCATCGGACGATGCTCATCATGATCAGGTAGCGCGACCTGGACACATTTACCTG 1320  
DB 1261 GCTTCATCGGACGATGCTCATCATGATCAGGTAGCGCGACCTGGACACATTTACCTG 1320  
OY 1321 TCGTGTCCAGCGGACGACGACCCCAATGGGCTGATCTGTGATGAGCTGACGATAT 1380  
DB 1321 TCGTGTCCAGCGGACGACGACCCCAATGGGCTGATCTGTGATGAGCTGACGATAT 1380  
OY 1381 GAGAAGAGCTCAGTGAATCAACGCGCACAGCCATATAAAAGCCCAACAGGTCAG 1440  
DB 1381 GAGAAGAGCTCAGTGAATCAACGCGCACAGCCATATAAAAGCCCAACAGGTCAG 1440  
OY 1441 GGCCTCAAGCCGCGCATCTATGCTTCCAGGTGGGCGACGACTGTGGAGGCTAC 1500  
DB 1441 GGCCTCAAGCCGCGCATCTATGCTTCCAGGTGGGCGACGACTGTGGAGGCTAC 1500  
OY 1501 GGGCGCTACAGGCGCAAGATGTACTTCCAGACATGACAGAGCCGAGTACAGACAAG 1560  
DB 1501 GGGCGCTACAGGCGCAAGATGTACTTCCAGACATGACAGAGCCGAGTACAGACAAG 1560  
OY 1561 ATCCAGAGAGTTCGACATCATCGGCTCTCGGCGCTGGCTGGCTCTCTCAT 1620  
DB 1561 ATCCAGAGAGTTCGACATCATCGGCTCTCGGCGCTGGCTGGCTCTCTCAT 1620  
OY 1621 GCTGTGTTGTATGCGCATCGTGTGTATACAGAGGGGGTGTAGGCTGTGACTGGAG 1680  
DB 1621 GCTGTGTTGTATGCGCATCGTGTGTATACAGAGGGGGTGTAGGCTGTGACTGGAG 1680  
OY 1681 TACAGGACAGCTGACACATCAACCAAGTGGCCACATAACCCAGGATGAAGATCTAC 1740  
DB 1681 TACAGGACAGCTGACACATCAACCAAGTGGCCACATAACCCAGGATGAAGATCTAC 1740  
OY 1741 ATGATCTCTTCACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
DB 1741 ATGATCTCTTCACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
OY 1801 GACATCTCTGTGTCAAAATTTGAGAGGTGATGAGAGGAGGAGGAGGAGGAGGAGGAG 1860  
DB 1801 GACATCTCTGTGTCAAAATTTGAGAGGTGATGAGAGGAGGAGGAGGAGGAGGAGGAG 1860  
OY 1861 AGTGGCCACCTGAGCTGCCAGGCAAGAGAGATCTTTGTGGCATCAAGAGCTCAAG 1920  
DB 1861 AGTGGCCACCTGAGCTGCCAGGCAAGAGAGATCTTTGTGGCATCAAGAGCTCAAG 1920  
OY 1921 TGGGGCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
DB 1921 TGGGGCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
OY 1981 TTGACCATCCCAAGCTATCCACTGAGAGGAGTGTGTGACCAAGAGACACCTGTGATG 2040  
DB 1981 TTGACCATCCCAAGCTATCCACTGAGAGGAGTGTGTGACCAAGAGACACCTGTGATG 2040  
OY 2041 ATCATACCGAGTTCAATGAGAAATGCTCCCTGACTCTTTCTCCGGCAAAACGATGGG 2100  
DB 2041 ATCATACCGAGTTCAATGAGAAATGCTCCCTGACTCTTTCTCCGGCAAAACGATGGG 2100  
OY 2101 CAGTTACAGTATCAGGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160  
DB 2101 CAGTTACAGTATCAGGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160  
OY 2161 CTGGGACATGAACTATGTACCGGTGACCTGGGCTGGCCGCAACATCTCTGTCAACAGC 2220

|    |      |  |      |
|----|------|--|------|
| Db | 2161 | CTGGCAGACATGAAACTATATTTCCACGGTGCACCTGGCTGCCCGCAACATCTCTGTCAAGAC  | 2220 |
| Oy | 2221 | AACCTGGTCGCAAGGTCGTGGACATTGGGGCTCTCACGCTTTCTTAGAAGACGATACCTCA    | 2280 |
| Db | 2221 | AACCTGGTCGCAAGGTCGTGGACATTGGGGCTCTCACGCTTTCTTAGAAGACGATACCTCA    | 2280 |
| Oy | 2281 | GACCCACCATAACACAGTGCCCTGGGCGGAAGTTTCCCATTCCGCTGCACAGCCCCGAA      | 2340 |
| Db | 2281 | GACCCACCATAACACAGTGCCCTGGGCGGAAGTTTCCCATTCCGCTGCACAGCCCCGAA      | 2340 |
| Oy | 2341 | GCCATCCATACCAGGAATTCACCTTCGGCCAGTGTGTGTGAGACTACGGCATTTGTATG      | 2400 |
| Db | 2341 | GCCATCCATACCAGGAATTCACCTTCGGCCAGTGTGTGTGAGACTACGGCATTTGTATG      | 2400 |
| Oy | 2401 | TGGGAGGTATGTCTCCATATGGGAGGGGCCCCATAGTGGGACATAGACAACCAAGATGTATC   | 2460 |
| Db | 2401 | TGGGAGGTATGTCTCTATGGGAGGGGCCCCCTTA CTGTTGGACATAGACAACCAAGATGTATC | 2460 |
| Oy | 2461 | AATGCCATTGACACAGACTATTCGGCTGCGCACCGCCCATGTAGACTCCCGAGGCCCTTGAC   | 2520 |
| Db | 2461 | AATGCCATTGACACAGACTATTCGGCTGCGCACCGCCCATGTAGACTCCCGAGGCCCTTGAC   | 2520 |
| Oy | 2521 | CAACATCATCTGAGACTGTGTGGAGAAGAACCGCAACCAACCGGCCCAAGTTGCGCCAATT    | 2580 |
| Db | 2521 | CAACTCATCTGTGACTGTGTGGAGAAGAACCGCAACCAACCGGCCCAAGTTGCGCCAATT     | 2580 |
| Oy | 2581 | GTCACACAGCTTAGACAMAGATGATCCGCAATCCCAACAGCCTCAAAGCCATGGCGCCCTTC   | 2640 |
| Db | 2581 | GTCACACAGCTTAGACAMAGATGATCCGCAATCCCAACAGCCTCAAAGCCATGGCGCCCTTC   | 2640 |
| Oy | 2641 | TCCTGTGCAATCAACCTGCGCGCTGCTGGACCGCACAGATCCCGCACTACACCACTTTAAC    | 2700 |
| Db | 2641 | TCCTGTGCAATCAACCTGCGCGCTGCTGGACCGCACAGATCCCGCACTACACCACTTTAAC    | 2700 |
| Oy | 2701 | ACGGTGGACGAGTGGCTGGAGGCGCATCAAGATGGGGAGTACAAGGAGACCTTCGGCAAT     | 2760 |
| Db | 2701 | ACGGTGGACGAGTGGCTGGAGGCGCATCAAGATGGGGAGTACAAGGAGACCTTCGGCAAT     | 2760 |
| Oy | 2761 | GCCGGCTTCACCTCCTTTGACAGTCGTCTCAGATGATGTGAGAGCAATTCGCGGTT         | 2820 |
| Db | 2761 | GCCGGCTTCACCTCCTTTGACAGTCGTCTCAGATGATGTGAGAGCAATTCGCGGTT         | 2820 |
| Oy | 2821 | GGGGTCACCTTTGGGCGGCACCAAAAAAATCTGAAACAGTATCCAGGTGATCGGCG         | 2880 |
| Db | 2821 | GGGGTCACCTTTGGGCGGCACCAAAAAAATCTGAAACAGTATCCAGGTGATCGGCG         | 2880 |
| Oy | 2881 | CAGATGAACAGATTCACTGTGTGGAGTTTGACATTCACCTCGCGGTCAACCTTC           | 2940 |
| Db | 2881 | CAGATGAACAGATTCACTGTGTGGAGTTTGACATTCACCTCGCGGTCAACCTTC           | 2940 |
| Oy | 2941 | CTCCAGGCCCGCGCCCTCTGC  | 2962 |
| Db | 2941 | CTCCAGGCCCGCGCCCTCTGC  | 2962 |

|                                   |  |
|-----------------------------------|--|
| RESULT                            | 3  |
| HUMREPKA                          |  |
| LOCUS                             |  |
| DEFINITION                        | HUMREPKA 2962 bp mRNA PRI 10-AUG-1995  |
| ACCESSION                         | L36643   |
| VERSION                           | L36643.1 GI:551609   |
| KEYWORDS                          | EPH-like receptor PTK; receptor protein-tyrosine kinase.   |
| SOURCE                            | Homo sapiens (clone library); Striatagene premade library, cat #93806) female fetus, 17-18 weeks gestation brain cDNA to mRNA. |
| ORGANISM                          | Homo sapiens   |
| Eukaryota;                        | Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;   |
| Mammalia;                         | Eutheria; Primates; Catarrhini; Hominiidae; Homo.  |
| 1 (bases 1 to 2962)               | Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M.,   |
| Babu,R. and Weicher,A.A.          | cDNA cloning and tissue distribution of five human EPH-like  |
| receptor protein-tyrosine kinases |  |

[illegible]

|    |      |   |      |
|----|------|---|------|
| QY | 1501 | GGGGCTACAGCGGCAGATGATCTTCCACATCATAGAGAAACCGAGTACCAAGCAAC          | 1560 |
| Db | 1501 | GGGGCTACAGCGGCAGATGATCTTCCACATCATAGAGAAACCGAGTACCAAGCAAC          | 1560 |
| QY | 1561 | ATTCAGGAGAACTGGCCACTCATCATCGCTCCGCGCCCTGGCTGGTCTTCTCATTT          | 1620 |
| Db | 1561 | ATTCAGGAGAACTGGCCACTCATCATCGCTCCGCGCCCTGGCTGGTCTTCTCATTT          | 1620 |
| QY | 1621 | GCTGTGGTTGTGCATCGCCATCGTGTGTAAACAGACGGGGGTTTAAAGCTGTGACTCGGGAG    | 1680 |
| Db | 1621 | GCTGTGGTTGTGCATCGCCATCGTGTGTAAACAGACGGGGGTTTAAAGCTGTGACTCGGGAG    | 1680 |
| QY | 1661 | TACACGGACGAAGCTGCGAACAACCTACACAGTGGCCACACTAAACCCAGGCAATGAAGATCTAC | 1740 |
| Db | 1661 | TACACGGACGAAGCTGCGACACTACACAGTGGCCACACTAAACCCAGGCAATGAAGATCTAC    | 1740 |
| QY | 1741 | ATTCATCTCTTTCACCTACAGAGAGACCCCAAGAGGCACTGGCGGAGTTTGGCCAAAGAAATT   | 1800 |
| Db | 1741 | ATTCATCTCTTTCACCTACAGAGAGACCCCAAGAGGCACTGGCGGAGTTTGGCCAAAGAAATT   | 1800 |
| QY | 1801 | GACATCTCTCTGTGTCAAAATTGACAGAGTGAATCGGACAGAGGGGAGTTTGGCGAGGCTGC    | 1860 |
| Db | 1801 | GACATCTCTCTGTGTCAAAATTGACAGAGTGAATCGGACAGAGGGGAGTTTGGCGAGGCTGC    | 1860 |
| QY | 1861 | AGTGGCCACTGGAAGCTCCAGCAAGAGAGATCTTTTGTGGCCATCAAGACGCTCAAG         | 1920 |
| Db | 1861 | AGTGGCCACTGGAAGCTCCAGCAAGAGAGATCTTTTGTGGCCATCAAGACGCTCAAG         | 1920 |
| QY | 1921 | TGCGGCTACAGCGAGAGCAGCGCGCGGAGCTTCTTGACCGCAAGCTTCATCATNTGGGCGAG    | 1980 |
| Db | 1921 | TGCGGCTACAGCGAGAGCAGCGCGCGGAGCTTCTTGACCGCAAGCTTCATCATNTGGGCGAG    | 1980 |
| QY | 1981 | TTTCGACCAATCCCAATGTCATGCACCTGAGAGGTCGTGAGACAGAGACACACCTGTGATG     | 2040 |
| Db | 1981 | TTTCGACCAATCCCAATGTCATGCACCTGAGAGGTCGTGAGACAGAGACACACCTGTGATG     | 2040 |
| QY | 2041 | ATCATACACCGAGTTCTANTGGAATGGCTCCCTGGACTCTCTTCTTCGCGCAAAACGATGGG    | 2100 |
| Db | 2041 | ATCATACACCGAGTTCTANTGGAATGGCTCCCTGGACTCTCTTCTTCGCGCAAAACGATGGG    | 2100 |
| QY | 2101 | CAGTTACAGTATCATCAGCTGGTGGGCAATGCTGGGGGCATCGGAGCGGATGAATAC         | 2160 |
| Db | 2101 | CAGTTACAGTATCATCAGCTGGTGGGCAATGCTGGGGGCATCGGAGCGGATGAATAC         | 2160 |
| QY | 2161 | CTGGGACAGATGAATATGTTTCAACGTCGACCTGGCTGCCCAACATCTCTGTAAACAGC       | 2220 |
| Db | 2161 | CTGGGACAGATGAATATGTTTCAACGTCGACCTGGCTGCCCAACATCTCTGTAAACAGC       | 2220 |
| QY | 2221 | AACCTGTCTGCAAGTGTGCGACTTTTGGGCTCTCAGCGTTTCTTAGAGAGACGATACCTCA     | 2280 |
| Db | 2221 | AACCTGTCTGCAAGTGTGCGACTTTTGGGCTCTCAGCGTTTCTTAGAGAGACGATACCTCA     | 2280 |
| QY | 2281 | GACCCACCTACACAGTGTCCCTGGGCGGAAAGTTTCCCATTCGCTGGACAGCCCCGGA        | 2340 |
| Db | 2281 | GACCCACCTACACAGTGTCCCTGGGCGGAAAGTTTCCCATTCGCTGGACAGCCCCGGA        | 2340 |
| QY | 2341 | GCCATCAGTACCGGAAAGTTTCACTTCGCGCAATGATGTGTGAGACTAGGCAATGTGATG      | 2400 |
| Db | 2341 | GCCATCAGTACCGGAAAGTTTCACTTCGCGCAATGATGTGTGAGACTAGGCAATGTGATG      | 2400 |
| QY | 2401 | TGGGAGGTATGTCATATGAGGGGAGGGCCCTACTGGGACATACCAACAGAGATTAATC        | 2460 |
| Db | 2401 | TGGGAGGTATGTCATATGAGGGGAGGGCCCTACTGGGACATACCAACAGAGATTAATC        | 2460 |
| QY | 2461 | AATGCATTGAGCAAGACATATGGGCTGCACCGCCCATGAGTGGCCCGAGCGCTTGAC         | 2520 |
| Db | 2461 | AATGCATTGAGCAAGACATATGGGCTGCACCGCCCATGAGTGGCCCGAGCGCTTGAC         | 2520 |
| QY | 2521 | CAACTCATGTGACACTGTGTGGCAGAAAGACCGAACCAGCCGGCCCAAGTTCCGCCAAATT     | 2580 |
| Db | 2521 | CAACTCATGTGACACTGTGTGGCAGAAAGACCGAACCAGCCGGCCCAAGTTCCGCCAAATT     | 2580 |
| QY | 2581 | GTCACACCGGTATACAAAGATGATCCGCATTCACACAGCCTCAAAAGCCATGGCGCCCTC      | 2640 |

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Db 2581 CTCACACCTTGAACAGATGATCGCAATCCCAAGCCTCAAAAGCATGGCCCCCTC 2640  
Oy 2641 TCTCTGGCATCAACCTGCGGCTGTGACCCGACAGATCCCGACATACACAGCTTTAAC 2700  
Db 2641 TCTCTGGCATCAACCTGCGGCTGTGACCCGACAGATCCCGACATACACAGCTTTAAC 2700  
Oy 2701 ACGGTGGACAGATGGCTGGAGGCCATCAAGATGGGGCACTACAGAGAGCTTCCCAAT 2760  
Db 2701 ACGGTGGACAGATGGCTGGAGGCCATCAAGATGGGGCACTACAGAGAGCTTCCCAAT 2760  
Oy 2761 GCCGGCTTACCTCTTACAGTCGTCACATGATGATGAGACATTTCTCCGGTT 2820  
Db 2761 GCCGGCTTACCTCTTACAGTCGTCACATGATGATGAGAGACATTTCTCCGGTT 2820  
Oy 2821 GGGGTCTACTTGGCTGGCCACCAAGAAAAATCTGACAGATATCCAGGTGATGGGGCG 2880  
Db 2821 GGGGTCTACTTGGCTGGCCACCAAGAAAAATCTGACAGATATCCAGGTGATGGGGCG 2880  
Oy 2881 CAGATGACACATTCAGTCTGTGAGGTTTGACATTCACCTGCTCGGCTACCTCTTC 2940  
Db 2881 CAGATGACACATTCAGTCTGTGAGGTTTGACATTCACCTGCTCGGCTACCTCTTC 2940  
Oy 2941 CTCGAAGCCCCCGCCCTCTGC 2962  
Db 2941 CTCGAAGCCCCCGCCCTCTGC 2962

RESULT 4  
AX034853 3768 bp DNA PAT 15-NOV-2000  
LOCUS AX034853  
DEFINITION Sequence 1 from Patent WO0053216.  
ACCESSION AX034853  
VERSION AX034853.1 GI:11190805  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3768)  
AUTHORS Vinals,Y.D.  
TITLE Novel uses  
JOURNAL Patent: WO 0053216-A 1 14-SEP-2000;  
SMITHKLINE BEECHAM BIOLOG (BE) ; VINALS Y DE BASSOLS CARLOTA (BE)  
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BASE COUNT 872 a 1129 c 1058 g 709 t  
ORIGIN

Query Match 98.7%; Score 2923.4; DB 9; Length 3768;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2956; Conservative 0; Mismatches 6; Indels 9; Gaps 2;

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RESULT 5  
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 mRNA, complete cds.  
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 VERSION DRT gene: EPH gene family; protein-tyrosine kinase.  
 KEYWORDS Homo sapiens (clone: FBK III 11c) (clone library: Stratagene,  
 Zapil, 936026) midterm fetus brain cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 3768)  
 AUTHORS Ikegaki,N., Tang,X.X., Liu,X.G., Biegel,J.A., Allen,C.,  
 Yoshioaka,A., Sulman,E.P., Brodeur,G.M. and Pleasure,D.E.  
 Molecular characterization and chromosomal localization of DRT  
 (EPH3): a developmentally regulated human protein-tyrosine kinase  
 gene of the EPH family  
 JOURNAL Hum. Mol. Genet., 4 (11), 2033-2045 (1995)  
 MEDLINE 96154673  
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ORIGIN

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Best local similarity 99.5%      Pred. No. 0;
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 VERSION D31661.1 GI:495677  
 KEYWORDS tyrosine kinase.  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS Iwase,T., Tanaka,M., Suzuki,M., Naito,Y., Sugimura,H. and Kino,I.  
 TITLE Identification of protein-tyrosine kinase genes preferentially  
 expressed in embryo stomach and gastric cancer  
 JOURNAL Biochem. Biophys. Res. Commun. 194 (2), 698-705 (1993)

REFERENCE  
 AUTHORS Kiyokawa,E., Takai,S., Tanaka,M., Iwase,T., Suzuki,M., Xiang,Y.Y.,  
 Naito,Y., Yamada,K., Sugimura,H. and Kino,I.  
 TITLE Overexpression of ERK, an EPH family receptor protein tyrosine  
 kinase, in various human tumors  
 JOURNAL Cancer Res. 54 (14), 3645-3650 (1994)

MEDLINE 94306360  
 TITLE 3 (bases 1 to 3151)  
 JOURNAL Kiyokawa,E.  
 DIRECT SUBMISSION  
 Submitted (23-MAY-1994) to the DDBJ/EMBL/Genbank databases. Etsuko  
 Kiyokawa, Hamamatsu University School of Medicine, First Department  
 of Pathology, 3600 Handa cho, Hamamatsu, Shizuoka 431-31, Japan  
 (Tel:81-53-435-2220, Fax:81-53-435-2225)  
 Submitted (23-May-1994) to DDBJ by:  
 Etsuko Kiyokawa  
 Hamamatsu University School of Medicine  
 First Department of Pathology  
 3600 Handa-cho  
 Hamamatsu, Shizuoka 431-31  
 Japan  
 Phone: 053-435-2220  
 Fax: 053-435-2225.

## COMMENT

COMMENT  
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 First Department of Pathology  
 3600 Handa-cho  
 Hamamatsu, Shizuoka 431-31  
 Japan  
 Phone: 053-435-2220  
 Fax: 053-435-2225.

## FEATURES

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Matches 2934; Conservative 0; Mismatches 13; Indels 9; Gaps 2;
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## RESULT 7

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LOCUS AX034855  
DEFINITION Sequence 3 from Patent W0053216.  
ACCESSION AX034855  
VERSION AX034855.1 GI:11190806  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 3949)  
AUTHORS Vinals, Y.D.  
TITLE Novel uses  
JOURNAL Patent: WO 0053216-A 3 14-SEP-2000;  
SMITHKLINE BEECHAM BIOLOG (BE) ; VINALS Y DE BASSOLS CARLOTA (BE)  
FEATURES  
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Query Match 97.4%; Score 2884; DB 9; Length 3949;  
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RESULT 8

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LOCUS Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA, complete cds.

ACCESSION AF025304

VERSION AF025304.1 GI:2739055

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3949)

AUTHORS Ikegaki,N., Tang,X.X., Liu,X.G., Biegel,J.A., Allen,C., Yoshioke,A., Sulman,E.P., Brodeur,G.M., and Pleasure,D.E.

TITLE Molecular characterization and chromosomal localization of DRT (EPHB2): a developmentally regulated human protein-tyrosine kinase gene of the EPH family

JOURNAL Hum. Mol. Genet. 4 (11), 2033-2045 (1995)

MEDLINE 96154673

REFERENCE 2 (bases 1 to 3949)

AUTHORS Tang,X.X., Pleasure,D.E., Brodeur,G.M., and Ikegaki,N.

TITLE A variant transcript encoding an isoform of the human protein tyrosine kinase EPHB2 is generated by alternative splicing and alternative use of polyadenylation signals

JOURNAL Oncogene 17 (4), 521-526 (1998)

MEDLINE 9696046

REFERENCE 3 (bases 1 to 3949)

AUTHORS Ikegaki,N. and Tang,X.X.

TITLE Direct Submission

JOURNAL Submitted (15-SEP-1997) Oncology, The Children's Hospital of Philadelphia, 324 South 34th Street, Philadelphia, PA 19104, USA

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BASE COUNT 934 a 1142 c 1105 g 768 t

ORIGIN

Query Match 97.4%; Score 2884; DB 88; Length 3949;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2903; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 1 CTCTGCGCGCGCGTGTAAGAAACGGTAATGGACTCACTACAGGACTGTGAGCTGGC 60

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Qy 61 TGGATGTCATCTCTCATCAGAGGTGGGAAGGTAGTGTCTACGATGAAACATGAAAC 120

Db 128 TGGATGTCATCTCTCATCAGAGGTGGGAAGGTAGTGTCTACGATGAAACATGAAAC 187

Qy 121 ACGATCCGACGTACCAAGGTGTCAACGCTTGTGATCAAGCAGAACATGCTAGC 180

Db 188 ACGATCCGACGTACCAAGGTGTCAACGCTTGTGATCAAGCAGAACATGCTAGC 247

Qy 181 ACGAAGTTATCCGGCGCGCGTGGGGCCCAACCGCATCCAGCTGAGATGAATTTCGGTG 240

Db 248 ACGAAGTTATCCGGCGCGCGTGGGGCCCAACCGCATCCAGCTGAGATGAATTTCGGTG 307

Qy 241 CGTACTGACAGACATCCCAAGCTGCTGGCTGGCAAGAGAGACTTCAACCTCTAT 300

Db 308 CGTACTGACAGACATCCCAAGCTGCTGGCTGGCAAGAGAGACTTCAACCTCTAT 367

Qy 301 TACTATGAGGCTGACTTGTGACTGGCCACCAAGACCTTCCCACTGATGGAATCCA 360

Db 368 TACTATGAGGCTGACTTGTGACTGGCCACCAAGACCTTCCCACTGATGGAATCCA 427

Qy 361 TGGGTGAAGTGAATACATTTGACGCCGAGAGAGAGCTTCCAGAGGAGCTGGGTGC 420

Db 428 TGGGTGAAGTGAATACATTTGACGCCGAGAGAGAGCTTCCAGAGGAGCTGGGTGC 487

Qy 421 CGCGCATGAATAATCAACACCGAGGTGGAGCTTCCGAGCTGTGTCGCGAGCGCTTC 480

Db 488 CGCGCATGAATAATCAACACCGAGGTGGAGCTTCCGAGCTGTGTCGCGAGCGCTTC 547

Qy 481 TACCTGGCTTCAGAGCATATGCGGCTGATGTCTCTCATCGCGCTGGCTGCTTCTAC 540

Db 548 TACCTGGCTTCAGAGCATATGCGGCTGATGTCTCTCATCGCGCTGGCTGCTTCTAC 607

Qy 541 CGCAAGTGGCGCGCATATCATCAGATGAGCGCATCTTCCAGAAACCTGTGGGGCT 600

Db 608 CGCAAGTGGCGCGCATATCATCAGATGAGCGCATCTTCCAGAAACCTGTGGGGCT 667

Qy 601 GAGAGCATATGCTGTGCTGCGCGGGGAGCTGATGCGCAATGCGGAAGAGTGGAT 660

Db 668 GAGAGCATATGCTGTGCTGCGCGGGGAGCTGATGCGCAATGCGGAAGAGTGGAT 727

Qy 661 GTACCATCAAGCTTCTACTGTAAAGGGGACGGGAGTGGCTGGTCCATCGGGCGCTGC 720  
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LOCUS Mus musculus Nuk receptor tyrosine kinase mRNA, complete cds.  
DEFINITION L25890.1 GI:414593  
VERSION 1  
KEYWORDS Nuk receptor tyrosine kinase.  
SOURCE Mus musculus Embryo cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3104)  
AUTHORS Henkemeyer M.  
TITLE Immunolocalization of the Nuk receptor tyrosine kinase suggests a  
role in segmental patterning of the brain and axonogenesis  
JOURNAL Oncogene (1994) In press  
FEATURES  
Location/Qualifiers  
1..3104  
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BASE COUNT 709 a 937 c 848 g 610 t  
ORIGIN

Query Match 84.3%; Score 2498; DB 94; Length 3104;  
Best local similarity 90.5%; Pred. No. 0;  
Matches 2679; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

QY 241 CGTACAGCAGACAGATCCCGAGCGTGCCTGCTCTCTGCAAGAGACCTTCACCTCAT 300  
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QY 301 TACTATGAGGCTGACTTTGACTGGCCACCAAGACCTTCCCAACTGATGAGAAATCCA 360  
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Db 1936 GAGGTGACAGTGGGCTTCACAGCTTCTGGCAAAAGAGATCTTTGTGGCATCAAG 1995  
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RESULT 11  
LOCUS 115008 4049 bp DNA PAT 02-Apr-1996  
DEFINITION Sequence 17 from patent US 5457048.  
ACCESSION 115008  
VERSION 115008.1 GI:1249916  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4049)  
AUTHORS Pasquale, E.B. and Sajjad, F.G.  
TITLE Eph-related tyrosine kinases, nucleotide sequences and methods of use  
JOURNAL Patent: US 5457048-A 17 10-OCT-1995;  
FEATURES  
source 1..4049  
location/Qualifiers  
BASE COUNT 1011 a 1010 c 1072 g 956 t  
ORIGIN

Query Match 73.8%; Score 2185.6; DB 10; Length 4049;  
Best Local Similarity 84.1%; Pred. No. 0;  
Matches 2493; Conservative 0; Mismatches 464; Indels 9; Gaps 2;

Oy 1 CTGCTCGCGCGCGTGAAGAAACCTAATGACTCCATCAGCAGCTGCTGAGCTGGC 60  
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Oy 541 CGCAAGTGGCGCGCATTCAGAAATGCGGCGCATTTCCAGAAACCTGTGCGGGGCT 600



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|----|------|---|------|
| Db | 616  | CGCAAGTGTCCCGTGTGATCCGAACGGGGGGTCTTCCAGGAAACCTCTCTGGGACGG         | 675  |
| QY | 601  | GAGAGCACAATGCGTGTGTGCTGTCCGGGGGACAGTTCATCGCCAAATGCGGAAGTGTGAT     | 660  |
| Db | 676  | GAGAGCAATCTCTGGTGGGAGCCCGGGGAGCTGCATCACCAATGCGGAGAGTGTGAT         | 735  |
| QY | 661  | GTACCACTCAAGCTCTACTGTATACGGGGGACGGCGAGTGGGCTGGTGGCCATCGGGCGCTGC   | 720  |
| Db | 736  | GTGGCCATCAAGCTGTACTGTCAATGGGGATGGCGAGTGGGTGTGGTCCATCGGCCCTGC      | 795  |
| QY | 721  | ATGTGCAAAACAGAGCTTCAGAGCCCTGTGTGAATGTGCACCGTCTGCGAGTGTGTCACT      | 780  |
| Db | 796  | ATGTGCAGGGCCGGGCTATAGTGTGGTGGGAATGTGGAGACCGTCTGGAGAGGCTGCCATCA    | 855  |
| QY | 781  | GGGACTTTCAAGGGCCACACAGGGGATGAGGCTGTACCACCTGTCCATCMAACAGCCGG       | 840  |
| Db | 856  | GGGACCTTCAAGGGCACCGCAAGAGATGGAAGATGTGTCCATTTGTCAATTAAACGCGG       | 915  |
| QY | 841  | ACCACTTGTGAAGGGGGCACCAACTGTGTCTGCGCCAAATGGCTACTACAGACAGACCTG      | 900  |
| Db | 916  | ACGACTTGGAAAGGGGCCACGAACTGCGTGTGCCGAAAGATATTACGGGGCAGATGCT        | 975  |
| QY | 901  | GACCCCTGTGACATGCCCCCTGCACACCAATCCCTCCGCGGCCAGGCTGTATTTCCAGT       | 960  |
| Db | 976  | GACCCCGTGCAGTGGCATGTACACACCAATCCCATCTGCCCCCGACGGCGGTATCTCCAGC     | 1035 |
| QY | 961  | GTCATATGACCTCCCTCATGTGTGAGTGTGAGCCCTCCCGCGAGCTTCGGAGGCCGGAAG      | 1020 |
| Db | 1036 | GTGAATGAACCTCTCGATGTGTGAGTGTGAGCCCAACACGAGACTTCAGGGGGCCGGGAG      | 1095 |
| QY | 1021 | GACCTGTGTCTCAACATCATCTGCACAAAGAGCTGTGCTCGGGCCGGGGTGCCTGCACCCG     | 1080 |
| Db | 1096 | GATCTGGAATCAACATCATCTGGAAGAGCTGTGGGTGCAGCGCTGTGGGCTGTGCACGCGC     | 1155 |
| QY | 1081 | TGCGGGGACAATGTACAGTACGACACACGCGACACTTAGGCTTCACCGAGCCACGCAATTAC    | 1140 |
| Db | 1156 | TGTGGGGCAACGTGCAAGATTTGGCCCCACGCACTGTGGCTTACGAGAGCTGTGGCACTTAC    | 1215 |
| QY | 1141 | ATCACTGTGACGTGTGTGGCCACACCCAGCTACACTTGTGAATCTCAGGCTGTGAACGGCGTT   | 1200 |
| Db | 1216 | ATTCAGCGACTGTGTGGCCACAGCGAGTACACTTTGAATTCAGAGCTGTGAATGGGCTC       | 1275 |
| QY | 1201 | ACTGACAGAGACCCCTTCTGCGCTCAGTTGTGCTGTGTAAATCATCACCAACACGAGCA       | 1260 |
| Db | 1276 | ACCGACAGAGACCCCTTCTCCCAAGATTTGTGATCAGTAAATATCACCAACCAAGGCT        | 1335 |
| QY | 1261 | GCTCCATGTGGAGTGTGTCATCATCAGTACAGGTGAGCGGACCGTGGACAGCTTACCCGTG     | 1320 |
| Db | 1336 | GGTCTTCAAGCGGTGTCCATATATCACACAGGTACGCGGCACTGTGTGACAGCACTTACCCCTC  | 1395 |
| QY | 1321 | TGCTGGTGTCCAGCCGAGACCAACCCAATGGCGGTATCCTGTGACTATGAGCTGTGACTATAT   | 1380 |
| Db | 1396 | TGCTGGTGTCAACCTGCAGCAGCCCAATGAGGTATCCTGTGATTATGAGCTGTGACTATAT     | 1455 |
| QY | 1381 | GAGAGGAGCTCATGTGATATACACGCCACACAGCATAAAAAGCCCGCAACCAACGGGTACG     | 1440 |
| Db | 1456 | GAGAGGAACCTGTAGGTAAATTCACACAGCAAGTGAAGGCCCCACCAACACTGTGACA        | 1515 |
| QY | 1441 | G-----GGCTCAAAAGCCGGGCGCATATGTCTTCCAGGTGTGGGCGACGCACTGTGCA        | 1494 |
| Db | 1516 | GTGCAAAACCTTAAGAGCTGTGCACCATCTATGTCTTCCAAAGTGTGGACACGTATACCGTGGCT | 1575 |
| QY | 1495 | GGCTAGGGGCGCTACAGCGGGAAGATGTACTTCCAGACATGACAGAGCCGAGTACAG         | 1554 |
| Db | 1576 | GGTATAGCGGTATAGTGTGCAAAATGTACTTCCAGACATGTACTGAACCCGAGTACAG        | 1635 |
| QY | 1555 | ACGAGATTCAGAGAAAGTGTGCACCTATCATATGTGGGTCCTGGGCGCTGTGGCTTC         | 1614 |
| Db | 1636 | ACCGAGTGTCAAGGAAGAGCTGTCACTATCTATGTGGCTCTCTCAGCAGAGACTGTGT        | 1699 |
| QY | 1615 | CTCATTTGCTGTGTGTGTATGTGCCATGTGTGTAAAC---AGACGGGGGTTTGAACCTGTCT    | 1671 |

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|----|------|---|------|
| Db | 1696 | CTCATTTGCTGTGTTGCTCTCATCATATTTATTTGTCTGCAACAGAAACACGGGGCTTTGAAACGTGCT | 1755 |
| Qy | 1672 | GACATCGAGATACAGGACAGCAAGCTGCAACCACTACACCACTGGCCACATPACCCAGCACTG       | 1731 |
| Db | 1756 | GACTCTGATGAACTGACAAAGCTGCGAGCAGCTATPACCACTGGCCCAATGACTCCACAGGATG      | 1815 |
| Qy | 1732 | AAGATCTACATCGATCTCTTTCACCTACGAGGAGCCCAACGAGGCGAGTGGAGATTGGC           | 1791 |
| Db | 1816 | AAGATTATATATGATCCATTTACTCTACAGAGATGCCCAATGAGGCTGTGCAGGAAATTTGCA       | 1875 |
| Qy | 1792 | AAGGAAATTGACATCTCCTGTGTCAAAATTTGACAGAGTATCGGAGCAAGGGAGTTTGGC          | 1851 |
| Db | 1876 | AAAGAAATTTGATATTCACCTCTGTGTGAAATATCGACAGGCTGATTGGGGCAGGGGAGATTGGT     | 1935 |
| Qy | 1852 | GAGGTCTGCAGTGGCCACCTGGAAGCTGCCAGGCACAGAGAGATCTTTGTGGCCATCAAG          | 1911 |
| Db | 1936 | GAGGTGTGCACGTGGGCAATCTCAAGCTTCTGTGCAAAAGAGATCTTTGTGGCCATCAAG          | 1995 |
| Qy | 1912 | ACGGTCAAGTGGGGCTTCACAGGAGACAGCGCCGAGGACTTCTGTAGCGAAGCCCTCATC          | 1971 |
| Db | 1996 | ACCCCTGAAGTGTGGTTTCACAGAGAAAGACAGACGGGAACTTCTAGTGAAGCCAGCATC          | 2055 |
| Qy | 1972 | ATGGGCCAGTTTGCACATTCCTCAACGCTATCCACCTGTGAGAGGTGTGTGTACCAACAGACA       | 2031 |
| Db | 2056 | ATGGGGCGATTGTGACATACCCCAATGTCTATCCACCTGGAAGGGGTGTGTATCCCAACAGATTCC    | 2115 |
| Qy | 2032 | CCTGTGATGATCATCACCGAGTTCATGAGAAATGGCTCCCTGTGACTCTCTTCTCCGGCAA         | 2091 |
| Db | 2116 | CCAGTCATGATCATTTACAGATTTATGTGAAATATGGCTGTGTGACTCTCTTGTAGGCAA          | 2175 |
| Qy | 2092 | AACGATGGGCGAGTTCCAGATCTATCCACGCTGTGTGGCATATCCCTTCCGGGGATGTGGCAGCTGAG  | 2151 |
| Db | 2176 | AATGATGTGGGAGTTTCCACAGATATCCACGCTGTGTGGCATATTCGTTGGGATTTGCGAGCA       | 2235 |
| Qy | 2152 | ATGAAGTACCTGGGCAACATGAATATGTTTACCGCTGACCTGGCTCCCGGCAACATCTCT          | 2211 |
| Db | 2236 | ATGAAGTACCTGGCTGATATGAACTACGTGACACCGGAGACTTGGCTCCCGCAACATCTCTG        | 2295 |
| Qy | 2212 | GTTCACACGACCACTGTGTGTGCAAGGTGTGGACTTTGGGCTCTCACGCTTTCTTAGAGAC         | 2271 |
| Db | 2296 | GTTCACAGAACTGTGTGTGTGCAAGGTGTCCGAACTTGGGCTCTCCGTTTCTGTGAGAT           | 2355 |
| Qy | 2272 | GATPACTCAGACCCACACTACACACAGTGGCCCTGGGGGAAAGTGTCCCATCGCTGAGCA          | 2331 |
| Db | 2356 | GACACTCTGATCCCACTTACACAGCGCACTGGGTGGAAAGATCCCAATGACGTGGAC             | 2415 |
| Qy | 2332 | GGCCGGGAAGCCATCAGTATACCGAATTCATCCTCGGCCAGTGAATGTGGAGCTTAGCGC          | 2391 |
| Db | 2416 | GGCCCTGAGGCAATTCATATACGAAATTCACATCAGCAGGATGTGGAGCTTATGGA              | 2475 |
| Qy | 2392 | ATTGTCTATGTGGAGGTATGCTCTATATGGGGACGGCCCTACTGGGACATGCAACACAG           | 2451 |
| Db | 2476 | ATAGTCTATGTGGAGGTATGTCTCTACGGGAGGGGCTTACTGGGACATGACCAATTA             | 2535 |
| Qy | 2452 | GATGTATCAATGACATTGAGCAGAGACTATCTGGCTGCAACCGCCATGAGTGCCTGAGC           | 2511 |
| Db | 2536 | GATGTATTAATGCTATTGTAGCAGAGACTATGTGGTACACACCCCTATGATTTGTCCAAT          | 2595 |
| Qy | 2512 | GGCCTTCACCACTATGCTTGTAGCTGTGGAGAGATGGAATCCACAGACCCCAAAATTT            | 2655 |
| Db | 2596 | GGCCTTCACCACTATGCTTGTAGCTGTGGAGAGATGGAATCCACAGACCCCAAAATTT            | 2655 |
| Qy | 2572 | GGCCTTCACCACTATGCTTGTAGCTGTGGAGAGATGGAATCCACAGCTCCAAACCATG            | 2631 |
| Db | 2656 | GGCCTTCACCACTATGCTTGTAGCTGTGGAGAGATGGAATCCACAGCTCCAAACCATG            | 2715 |
| Qy | 2632 | GGCCTTCACCACTATGCTTGTAGCTGTGGAGAGATGGAATCCACAGCTCCAAACCATG            | 2691 |
| Db | 2716 | GGCCTTCACCACTATGCTTGTAGCTGTGGAGAGATGGAATCCACAGCTCCAAATATAC            | 2775 |
| Qy | 2692 | AGCTTTAACAAGGTGACAGAGTGGCTGGAGGCCATCAAGATGGGGAGATGCAAGAGAGAC          | 2751 |
| Db | 2776 | AGCTTTAACAAGGTGATGAATATGGCTGGATCCCAATCAAGATGAGCCAGTACAAAGAGAGAC       | 2835 |



Db 946 GACCTGTGACATGCCATGCAACCACTCCATTCGCCCCCACTCCGTATCTCCAGT 1005  
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Db 1486 GTGCAAAACCTCAAAAGCTGTGACACATCTACGCTTCCAAAGTGCAGACGATACCGGCT 1545  
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Qy 1555 AACAGCATCAGAGAGAAATGGCACTCATGCGCTCCGCGCTGGCGCTGCTTC 1614  
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Db 1726 TCGAGTACAGAGAGAGTGCACATGACAGTGGCCACATGACCTCTGGAGTGAAG 1785  
Qy 1735 ATCTACATGATCTTTCACTACAGAGACCCCAACAGAGCAAGTGGGAGTTGGCAAG 1794  
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Qy 1795 GAAATGACATCTCTGTGTCAAAATTTGAGCAGGTATGGGAGCAGGAGTTGGCGAG 1854  
Db 1846 GAAATGATATCTCTGTGTGAATAATGAGAGGTGATTGGGGCAGGAGTTGGTGTG 1905  
Qy 1855 GTCTGAGTGGGACCTGAGAGTGCAGGCAAGAGAGATCTTTTGGCCATCAGAG 1914  
Db 1906 GTGTGAGTGGGACCTGCAAGCTTCTGGCAAAAGAGATCTTCTGGCCATCAGAG 1965  
Qy 1915 CTCAAGTGGGGCTACAGGAGAGAGCGCCGGGACTTCTTGAGGAGAGCTTCATATG 1974  
Db 1966 CTCAAGTGGGGCTACAGGAGAGAGCGGAGATTTCTTGAGGAGAGCTTCATATG 2025  
Qy 1975 GGCAGTGTGACATCCCAAGCTACCACTGAGAGGTGTGTGACCAAGACACACCT 2034  
Db 2026 GGACAGTGTGTATCCCAAGCTACCACTGAGAGGTGTGTGACCAAGAGTTCCTCA 2085

Qy 2035 GTGATGATCATCACCGAGTTTCATGAGAGATGGCTCCCTGGACTCTTTCCTCCGCAAAAC 2094  
Db 2086 GTCAATGATTAATTAACGAGTTTATGAGATGGCTGTGTGGACTCTTCTTGAAGCAAAAC 2145  
Qy 2095 GATGGGAGTTCACAGTCAATCAGTGTGTGGCAATGCTTCGGGGCAATCGACGTGGCATG 2154  
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Db 2506 GTATCAATGCCATTTAGCAGAGTATCGGCTGCCACCGCCATGAGCTGCCAGCGCC 2565  
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Db 2866 CCGGTTGGGCTACCTTGTGCTGGCCACAGAAATAATCTTAACAGTATCCAGGTGATG 2925  
Qy 2875 CCGGCGCAGATGACAGATGATGATGTGTGAGGTTTGAATTCACCTGCGCTGAC 2934  
Db 2926 CCGGCGCAGATGACAGATGATGATGTGTGAGGTTTGAATTCACCTGCGCTGAC 2985  
Qy 2935 CTCTTCTCTCAAGCCCGCCGCC 2957  
Db 2986 CACTTCTCTTGAAGCCCTGCTCC 3008

RESULT 13  
LOCUS 115005 4097 bp DNA  
DEFINITION Sequence 11 from patent US 5457048. PAT 02-APR-1996  
ACCESSION 115005  
VERSION 115005.1 GI:1249913  
KEYWORDS



|    |      |   |      |
|----|------|---|------|
| OY | 1864 | GGCACCTGAAGTGTGCAGAGCAAGAGAGATCTTTGGGCACTCAACAGCTCAAGCG       | 1923 |
| OY | 1864 | GGCACCTGAAGTGTGCAGAGCAAGAGAGATCTTTGGGCACTCAACAGCTCAAGCG       | 1923 |
| Db | 1996 | GGGATCTCAAGTCTCTGGCAAAAGAGATCTTTGGGCACTCAACAGCTCAAGCT         | 2055 |
| OY | 1924 | GGCATACAGAGAGAGCAAGCGCCGGGACTTCTGAGCGAAGCCCTCATCATGGGCAATT    | 1983 |
| Db | 2056 | GGTTACACAGAGAGAGAGAGAGAGCTCTGAGTGAAGGACGACATCATGGGCAAGTT      | 2115 |
| OY | 1984 | GACCATCCCAAGTCACTCACTGGAGGGGTGTCTGACCAAGACAGCAACCTGATGATC     | 2043 |
| Db | 2116 | GACACCCCAATGTCAATCCACTGGAAAGGGGTGTGACCAAGATTTCCCAAGTATGTG     | 2175 |
| OY | 2044 | ATCACCGATTCATGAGAGTGGCTCCCTGGACTCTCTTCGCGCAAAACGATGGGAC       | 2103 |
| Db | 2176 | ATTACAGATTCATGAGAGTGGCTGTTGGACTCTCTTGAAGCAAAATGATGGGAC        | 2235 |
| OY | 2104 | TTACAGTCACTCAAGCTGTGGGCACTGCTTCGGGGCATCGACGCTGGCATGATACCTG    | 2163 |
| Db | 2236 | TTACAGTCACTCAAGCTGTGGGCACTGCTTCGGGGCATCGACGCTGGCATGATACCTG    | 2295 |
| OY | 2164 | GCACACATGAACATATGTTACCGTGAACCTGGGCTGGCCCGCAACATCTGTGAACGCAAC  | 2223 |
| Db | 2296 | GCTGATATGAACATCACTGTCACCGGGAACCTGGCTGCCCGCAACATCTGTGAACGCAAC  | 2355 |
| OY | 2224 | CTGGCTTCGAAGGTGTGCGACTTTGGGCTCTCAAGCTTCTAGAGAGCATCTCAGAC      | 2283 |
| Db | 2356 | CTGGCTTCGAAGGTGTGCGACTTTGGGCTCTCAAGCTTCTAGAGAGCATCTCAGAC      | 2455 |
| OY | 2284 | CCCACTACACACATGCCCCGGGCGGAAAGTTCCCATCGCTGGACAGCCCGGAAACC      | 2343 |
| Db | 2416 | CCCACTACACACACATGCCCCGGGCGGAAAGTTCCCATCGCTGGACAGCCCGTGAAGCA   | 2475 |
| OY | 2344 | ATTCAGTACCGGAGTTCACCTCTCGGCGCAGTATGTGTGAGGTACGCAATTGTCTATGG   | 2403 |
| Db | 2476 | ATTCAGTACCGGAGTTCACCTCTCGGCGCAGTATGTGTGAGGTACGCAATTGTCTATGG   | 2535 |
| OY | 2404 | GAGTGATGTCTTATGGGAGACGGCTTACTGGGACATGACCAACAGGATGATCAAT       | 2463 |
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| OY | 2464 | GCCATTGGACAGGACTTTCGGCTTCCACCGCCCATGAGCTGCCCGGACCCCTGCACCA    | 2523 |
| Db | 2596 | GCCATTGGACAGGACTTTCGGCTTCCACCGCCCATGAGCTGCCCGGACCCCTGCACCA    | 2655 |
| OY | 2524 | CTCATGCTGACCTGTGGCAGAAAGACCGACACCCAGCGGCCAAGTTGCGGCAAAATGTTC  | 2583 |
| Db | 2656 | CTCATGCTGACCTGTGGCAGAAAGACCGACACCCAGCGGCCAAGTTGCGGCAAAATGTTC  | 2715 |
| OY | 2584 | AACAGCTAGACAAAGATGATCCGAATCCCAACAGGCTCAAAAGCCATGTGCGCCCTTCC   | 2643 |
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OY      2944  CAAGCCCGGCGCC 2357
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Db      3076  GAGGCCCTGCTGCC 3089

RESULT 14
AF026039      2664 bp      mRNA      VRT      08-JUN-1999
LOCUS      Xenopus laevis Ephb2-tyrosine kinase receptor (xephb2) mRNA,
DEFINITION      partial cds.
ACCESSION      AF026039
VERSION      AF026039.1
KEYWORDS      GI:2739061
SOURCE      African clawed frog.
ORGANISM      Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE      1 (bases 1 to 2664)
AUTHORS      Tanaka,M., Wang,D.Y., Kamo,T., Igarashi,H., Wang,Y., Xiang,Y.Y.,
              Tanioka,F., Naito,Y. and Sugimura,H.
              Intersection of Ephb2-tyrosine kinase receptor and its ligand
              conveys dorsalization signal in Xenopus laevis development
              oncogene 17 (12), 1509-1516 (1998)

JOURNAL      JOURNAL
MEDLINE      99008330
PUBMED      9794228
REFERENCE      2 (bases 1 to 2664)
AUTHORS      Wang,D.Y. and Tanaka,M.
TITLE      Direct Submission
JOURNAL      Submitted (18-SEP-1997) First Department of Pathology, Hamamatsu
              University School of Medicine, 3600 Handa-cho, Hamamatsu, Shizuoka
              431-31, Japan

FEATURES
source      Location/Qualifiers
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RESULT 15  
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LOCUS Homo sapiens (clone FBK III 16) protein tyrosine kinase (NET PK)  
DEFINITION mRNA, complete cds.  
ACCESSION L40636.1 GI:1100111  
VERSION L40636.1  
KEYWORDS NET PK gene; neuronal differentiation; protein-tyrosine kinase.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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CDNA cloning, molecular characterization, and chromosomal  
localization of NET(PHPT2), a human EPH-related receptor  
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Genomics 29 (2), 426-437 (1995)  
96115594

JOURNAL MEDLINE  
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Db 3081 TAGGATCATCCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3140
Oy 2879 CGCAATGACCAAGATTAAGTGTGTGAGAGTGTGA 2915
Db 3141 TCAGATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3177

```

Search completed: July 10, 2001, 17:59:33  
 Job time: 10295 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 16:52:23 ; Search time 195.92 Seconds

(without alignments)  
9492.878 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CTCGCGCCGCCGCTGGAAGA.....CCAAAGCCCCCCTCTGC 2962

Scoring table: IDENTITY\_NUC  
Gapext 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1          | 2962   | 100.0       | 2962   | 16 | AA02946     |
| 2          | 2923.4 | 98.7        | 3768   | 21 | AA088548    |
| 3          | 2897.2 | 97.8        | 3151   | 21 | AA009322    |
| 4          | 2884   | 97.4        | 3949   | 21 | AA088549    |
| 5          | 2498   | 84.3        | 3105   | 18 | AA084528    |
| 6          | 2496.4 | 84.3        | 3105   | 16 | AA07308     |
| 7          | 2187.2 | 73.8        | 4049   | 16 | AA090660    |
| 8          | 2127.6 | 71.8        | 4097   | 16 | AA090657    |
| 9          | 1631   | 55.1        | 4281   | 14 | AA053471    |
| 10         | 1583.4 | 53.1        | 3751   | 15 | AA062461    |
| 11         | 1581.6 | 53.4        | 3546   | 16 | AA090656    |

|    |        |      |      |    |          |                    |
|----|--------|------|------|----|----------|--------------------|
| 12 | 1543.4 | 52.1 | 3591 | 16 | AA090658 | Eph-related PTK Ce |
| 13 | 1526.4 | 51.5 | 4027 | 16 | AA090972 | Protein p140 CDNA  |
| 14 | 1526.4 | 51.5 | 4027 | 16 | AA090982 | Protein p140 CDNA  |
| 15 | 1520.8 | 51.3 | 2982 | 16 | AA090971 | Protein p140 CDNA  |
| 16 | 1469.6 | 49.6 | 3133 | 16 | AA090652 | Eph-related PTK Ce |
| 17 | 1196.8 | 40.4 | 3776 | 16 | AA090655 | Eph-related PTK Ce |
| 18 | 1075   | 36.3 | 3969 | 16 | AA090659 | Human non-differen |
| 19 | 1073.4 | 36.2 | 4290 | 16 | AA092641 | Receptor-tyrosine  |
| 20 | 1073.4 | 36.2 | 4290 | 17 | AA092641 | Coding sequence fo |
| 21 | 1073.4 | 36.2 | 4290 | 18 | AA092641 | Receptor-tyrosine  |
| 22 | 1072.4 | 35.9 | 3969 | 17 | AA092641 | Receptor-tyrosine  |
| 23 | 1067.2 | 35.9 | 4290 | 17 | AA092641 | Receptor-tyrosine  |
| 24 | 1037.2 | 35.0 | 3116 | 16 | AA092648 | Eph-related PTK Ce |
| 25 | 1035.6 | 35.0 | 3348 | 16 | AA093100 | Eph-related PTK Ce |
| 26 | 992.8  | 33.5 | 3254 | 16 | AA090659 | Eph-related PTK Ce |
| 27 | 956.8  | 32.3 | 3162 | 16 | AA092647 | Eph-related PTK Ce |
| 28 | 949.4  | 32.1 | 2820 | 16 | AA090654 | Eph-related PTK Ce |
| 29 | 943.8  | 31.9 | 4304 | 17 | AA092660 | Mouse developmenta |
| 30 | 917.6  | 31.0 | 3300 | 21 | AA064459 | CDNA encoding a hu |
| 31 | 912.8  | 30.8 | 3149 | 21 | AA064458 | CDNA encoding a hu |
| 32 | 907    | 30.6 | 4529 | 16 | AA092649 | Eph-related PTK Ce |
| 33 | 906.4  | 30.6 | 3132 | 14 | AA034513 | HEK coding sequenc |
| 34 | 869    | 29.3 | 3906 | 20 | AA070207 | Human thymus recep |
| 35 | 800.8  | 27.0 | 4022 | 19 | AA062177 | Human thymus recep |
| 36 | 799.2  | 27.0 | 3673 | 19 | AA062177 | Human thymus recep |
| 37 | 743    | 25.1 | 3367 | 21 | AA093697 | Human thymus recep |
| 38 | 735.4  | 24.8 | 1509 | 14 | AA053470 | CDNA encoding huma |
| 39 | 723    | 24.4 | 2170 | 20 | AA041307 | Human normal ovary |
| 40 | 697.2  | 23.5 | 3592 | 20 | AA070208 | Rat receptor tyros |
| 41 | 661.2  | 22.3 | 3059 | 16 | AA090653 | Eph-related PTK Ce |
| 42 | 629.6  | 21.3 | 3056 | 16 | AA090662 | Eph-related PTK Ce |
| 43 | 605.2  | 20.4 | 3125 | 16 | AA090661 | Eph-related PTK Ce |
| 44 | 572.8  | 19.3 | 4165 | 17 | AA018993 | Rat REK7 CDNA. Ra  |
| 45 | 564    | 19.0 | 4322 | 19 | AA058192 | Mouse Bsk receptor |

#### ALIGNMENTS

|          |  |                          |
|----------|--|--------------------------|
| RESULT 1 | AA02946  | standard: CDNA; 2962 BP. |
| ID       | AA02946  | standard: CDNA; 2962 BP. |
| AC       | AA02946  |                          |
| DT       | 16-APR-1996  | (first entry)            |
| DE       | EPH-like receptor protein tyrosine kinase HEK5 CDNA.             |                          |
| KW       | EPH-like receptor protein tyrosine kinase; PTK; HEK5;            |                          |
| KW       | human eph-like kinase; therapy; diagnosis; antibody; vector; ss. |                          |
| OS       | Homo sapiens.  |                          |
| FT       | Key  | Location/Qualifiers      |
| FT       | CDS  | 1..2913                  |
| FT       |  | /*tag= a                 |
| PN       | W09528484-A1.  |                          |
| PD       | 26-OCT-1995.   |                          |
| PF       | 14-APR-1995;   | 95WO-US04681.            |
| PR       | 15-APR-1994;   | 94US-0229509.            |
| PA       | (AMGE-) AMGEN INC.   |                          |
| PI       | Fox GM, Jing S, Welcher AA;                                      |                          |
| DR       | WPI; 1995-373799/48.   |                          |
| DR       | P-PSDB; AAR85089.  |                          |
| XX       |  |                          |



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Db 1861 agtggcaccctgtagctgccaagcagaagagatactttgtgccaatcaagaagcttcaag 1920
QY 1921 TCGGCGTTACACGGAGAGACGCGCGGACCTTCTAGACGCAACCTCCATCATGGGCCAG 1980
Db 1921 tcgggtctacacgagagaagcagcgccgggacttctctgagcgaagcctccatcalggccag 1980
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Db 2041 atcatcaccgagttctatgagaaatggctccctgagactcttctccggcaaaagatggg 2100
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Db 2221 aaactgtctcgaaggtgtcgcgacttgggctctacagcttcttgaagagcgttacctca 2280
QY 2281 GACCCCACTACACAGTGGCTGGCGGCAAAATTCCTCCATCCCTGAGACAGCCCGGAA 2340
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Db 2341 gccatcagtagcagagattcaacctcgccagtgatgtgtgagatcaggtcatgtgcaag 2400
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Db 2461 aatgccattgagagagactatggctgccacccgcatgagtagctgcgagccgctgac 2520
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Db 2881 cagatgaaccagattcagttctgtgaggtttgacattcaccctgcctgcctcacctcttc 2940
QY 2941 CTCGAAGCCCCGCCCTCTGC 2962
Db 2941 ctccaagccccgccctctgc 2962

RESULT 2
AAA88548
ID AAA88548 standard; cDNA; 3768 BP.
XX
AC AAA88548;
XX
DT 22-JAN-2001 (first entry)
XX
DE Human CASB616 cDNA.
XX
KW CASB616; EPHB2; ERK; EPH3; EPH3T3; DRT; HEK5; EPHB2V;
KW receptor protein tyrosine kinase; human; antigen; colon cancer;
KW ovary cancer; tumour; autoimmune disease; vaccine; gene therapy;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 105..3068
FT FT /tag= a
FT /transl_except= (pos:2973..2975,aa:Leu)
PN MO200053216-A2.
XX
PD 14-SEP-2000.
XX
PF 28-FEB-2000; 2000MO-BE01587.
XX
PR 05-MAR-1999; 99GB-0005124.
XX
PA (SMRK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Vinals De Bassols YC;
XX
DR WPI: 2000-587384/55.
XX
DR P-PSDB; AAB19590.
XX
PT Vaccine composition for treating ovarian and colon cancer, comprises
PT CASB616 polypeptides, polynucleotides or antigen presenting cells
PT expressing the polypeptides
XX
PS Claim 3; Page 40-41; 57pp; English.
XX
CC The present sequence is that of cDNA coding for human CASB616 (see
CC AAB19590), a member of the EPH and EPH-related family of receptor
CC protein tyrosine kinases. CASB616 is also known as EPHB2, ERK,
CC EPH3, EPH3T3, DRT, HEK5 and EPHB2V. CASB616 polypeptides and
CC polynucleotides are important immunogens for specific prophylactic
CC or therapeutic immunization against tumours, especially colon
CC cancer (claimed) and ovarian cancer. They are specifically
CC expressed or highly over-expressed in tumours compared to normal
CC cells and can thus be targeted by antigen-specific immune
CC mechanisms leading to destruction of the tumour cells. They can
CC also be used to diagnose the occurrence of tumour cells. Their
CC inappropriate expression can also cause an induction of autoimmune
CC responses, which can be corrected through vaccination using the
CC CASB616 polypeptides or polynucleotides.
XX
SQ Sequence 3768 BP; 872 A; 1129 C; 1058 G; 709 T; 0 other;

Query Match 98.7%; Score 2923.4; DB 21; Length 3768;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2956; Conservative 0; Mismatches 6; Indels 9; Gaps 2;
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Db 207 tggatggtgcatctccatccatcaggttgaagaaggttgaatggtactaagatgaacaatgaac 266  
OY 121 ACGATCCGACGATACCCAGTGTGCAACGCTTTGATGATCAACGCAACAACTGGGTAGGC 180  
Db 267 aagatccgcacgtaccaggtgtgaacglttltgaagtcacagcagaacaactggtactagc 326  
OY 181 ACCAAGTTTATCCGGCGCGCTGGGGCCACCGCATCCAGTGGAGATGAAGTTTTCGGTGG 240  
Db 327 accaagttatccggtgcgcgtggtggccacgcgtaccatccatcagatgaatglttccgttg 386  
OY 241 CGTGACTGCAGACGATCCCAAGCGCTGCTGCTTCCTCAAGAGAGACCTTCAACTCTAT 300  
Db 387 cgtgactgcagagatcccatccagcgtgcttgccttgcaagagaaacttcaactctat 446  
OY 301 TACTATGAGCGTGAATTTGACCTGGGCGCACCAAGACCTTCCCAACTGGATGGAGAAATCA 360  
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Db 507 tgggtgaaggtgtgataccattgacgtcagcgcagcagagacttctcccaagtgtgacctgtg 566  
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Db 567 cgcgtcatgaataataaaccgaaggtgcgaagcttcggaacctgtgtccgcgcgcgtcttc 626  
OY 481 TACCGGCGCTTCCAGAGACTATGAGCGCTGACATGTCCTCATCGCGCTGCTGCTTCTTAC 540  
Db 627 tactcgtgccttccaggaataatgtggtgcgtgtcatgttccctcatccgtgtgtcttctac 686  
OY 541 CGCAAGTCCCGCGCATCATCCAGAAATGGCGCATTTTCAAGAAACCTGTGGGGGCT 600  
Db 687 cgaagtgccccgcgcatcatccagaatgtgcacatcttccagaacacctgtcggggct 746  
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OY 721 ATGTGCAAGACGAGCTTGAAGGCGCTTGAGAAATGGCACCGTGTGCGAGTTGCTCATCT 780  
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OY 841 ACACCTTCTGAAGGGGCCACCAACTGTGTGTGCGCAATGGCTACTACAGACAGACCTG 900  
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OY 961 GTCATGAGACCTCCCTATGCTGAGTGGAGGACCCCTCCCGGAGTCCGGAGCGGAGAG 1020  
Db 1107 gtcaatgagacctccctcatatgt 1166  
OY 1021 GACCTGTCTACAAACATCATCTGCAAGAGCTGTGGCTGGGGCGGGGCTGCTGACCGGC 1080  
Db 1167 gacctgtctacaacatcatctgtcaagagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1226  
OY 1081 TGGGGGGAATGTACAGTACGACACCAAGCTTAGGCTGTACCGAGGACGCAATTAC 1140  
|||||

|||||  
Db 1227 tgcggggacaatgtacagtaacacacgcagctaggtgcctgaccagagccaacatllac 1286  
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Db 1287 atcagtacacctgt 1346  
OY 1201 ACTGACCGAGAGCCCTTTCGCGCTGAGTTCGCTGTGTGAACATCAACCAACCAAGCACA 1260  
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Db 1407 gctccatcggcaggtgttccatcatatgcatcaggtgtgagccgaccgtgtgacagatllacctg 1466  
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Db 1707 acaagcatccaggaaggt 1766  
OY 1615 CTCATTGCTGT 1671  
Db 1767 ctcatltgt 1826  
OY 1672 GACTCGAGTACAGGAGACGACGTCGACACACTGAGTGGCGCATTAACCCAGGACATG 1731  
Db 1827 gactcggagttacaggaacagctgt 1886  
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OY 2272 GATACCTCAGACCCACCTACACAGTGGCCCTGGGCGAAAGTTCCCAATCCGCTGGACA 2331
DB 2427 gatccctcagaccccaacctacacagtgccctggcgaaagatccccaatccgctggaca 2486
OY 2332 GCGCCGGAAGCCATCGATACCGGAAGTTCACTCGGCATGATGTTGTGAGCTAGCGC 2391
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DB 2667 gccctgcaccaactcatctgactgttgagagagacgcgcaacacgcgcgcagcttc 2726
OY 2572 GGGCAATTGTCAACAGCGTAAAGATGATCCGCAATCCCAACAGCTTCAAGCCATG 2631
DB 2727 gggcaaatgtcacagcgtaagatgattccgcgaatcccaacagcttcaagccatg 2786
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DB 2787 gcgcctctctctctgtgcatacaacctgcgcgtgtgagacgcgcaagatcccgactacac 2846
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OY 2932 CACCTCTTCTCCAAAGCCCGCCCTCTGCG 2962
DB 3087 cacctctctctcagaagcccgccctctcgc 3117

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RESULT 3  
 AAA09322 standard; DNA; 3151 BP.  
 AAA09322;

10-AUG-2000 (first entry)  
 Human cancer associated antigen precursor DNA, clone NY-REN-47.  
 renal cancer; cancer associated antigen precursor; diagnosis;  
 cytosolic; ERK tyrosine kinase; ss.  
 Homo sapiens.  
 MO200020587-A2.  
 13-APR-2000.

PF 04-OCT-1999; 99MO-US22873.  
 XX  
 PR 05-OCT-1998; 98US-0166300.  
 PR 05-OCT-1998; 98US-0166350.  
 XX  
 PA (LUDWIG INST CANCER RES.  
 PI Ohta Y, Gout I, Tureci O, Sahin U, Pfreundschuh M, Scanlan MJ;  
 PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A.  
 DR WPI: 2000-303774/26.  
 XX  
 PT Preventing, diagnosing and/or treating disorders associated with  
 PT abnormal expression of human cancer associated antigens  
 PS  
 PS Claim 57; Page 93-94; 121pp; English.

CC AAA09321-45 were isolated by SEREX screening from a renal cancer  
 CC cell line 1973/10.4. Homology searching revealed that these clones  
 CC correspond to known genes. The present sequence has identity with the  
 CC ERK tyrosine kinase gene. The genes encode cancer associated antigen  
 CC precursors. These gene products are useful in methods for preventing,  
 CC diagnosis and/or treating disorders, especially cancer, associated with  
 CC abnormal expression of human cancer associated antigens. The method  
 CC comprises contacting a sample from a subject with an agent that  
 CC specifically binds to the nucleic acid molecule or expression product  
 CC (or fragment) complexed with a human leukocyte antigen (HLA) molecule  
 CC and determining the interaction between the agent and the nucleic acid  
 CC molecule or the expression product as a determination of the disorder.  
 XX  
 SQ Sequence 3151 BP; 707 A; 974 C; 874 G; 566 T; 0 other;

Query Match 97.8%; Score 2897.2; DB 21; Length 3151;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 2934; Conservative 0; Mismatches 13; Indels 9; Gaps 2;

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DB 124 ccattcaggctgggaagagtgaatgctgctacgattgagaaacatgaacagatccgcagctac 183
OY 136 CAGGTGCAACGTTTGAATGATCAAGCAACAGTGGCTAGGACCAAGTTATCCG 195
DB 184 caggtgcaacgtttgaaatgattcaagcaacagtggctaggacccaagttatccgg 243
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DB 244 cgcggtggggccacccgcatccagtggaagtgaatttcgctgctgctgctgctgctgctgctg 303
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2227 GGTGTCAAGGTGTCGACTTGTGGCTTCACGCTTTCATGAGAGAGATACCTCAGACCC 2286
2284 ggtgtcaaggtgtcgtactgtgtgtctcacaagcttcttagaagaatacctcagaacccc 2343
2287 ACCTACACCAAGTCCCTGGGGGCAAAATTTCCCATTCGCTGTGACAGCCCGGAAACCATC 2346
2344 acctacaccaagtgcccttggygcgaagaatccccatctgcgtgacacgcccgyaagccatc 2403
2347 CAGTACCGGAAGTTCACTCGGCGCAAGTGATGTGAGACTGAGCATTTGCTATGTGGAG 2406
2404 cagtagtccctatgggagggcgccctacttgagacatgacacacagagatgtaatgagcc 2466
2407 GTGATGCTCTATGGGAGGCGGCTTACTGAGACATGACCAACAGAGATGTAATCAATGCC 2466
2464 gtgagtctctatggygaggygcctactgtggaatgacacacagatgttaatcaatgccc 2523
2467 ATTGACGAGACTATCGCTGCCACCGCCATGAGACTGCCCGCAGCGCCTGTGACCAATC 2526
2524 attgagcagactatcgtgtgcacgcgcccacgtactgcccagctgtcctgtgacaactc 2583
2527 ATGCTGGAGTGTGGTAGAAGACCGCAACACCGGCCCAAGTGGGCCCAATTTGCAAC 2586
2584 atgctggagtgttggtagaagacgccaacacgcgcccagatctgccaatgttcaaac 2643
2587 ACGCTGACAAAGATGATCGCAATCCCAACAGCCTTCAAAGCCATGGCGCCCTCTCTCT 2646
2644 acgtgtaagaagatgtatccgcaatcccaacagctctcaagaacatgtgcccctctcctct 2703
2647 GGCATCAACCTGCGCTGTGTGACCGCACGATCCCGACTACCAACAGCTTTAAACAGG 2706
2704 ggcataacctgscgtgtgtgacccgcacgatccccgataacacagcttataacagtg 2763
2707 GACGATGGCTGAGGCGCATCAAGATGGGGGAGTCAAGAGAGCTTGGCCATGCGCGGC 2766
1687 gtgtgcatcgcatcgtgtgttaacagacggyggttggcgctgtcgtacgtgagtaacg 1743
1687 gacaagctgcaaaccttaacacagtggtcacatgacatgacccaagatgaatctacatcgat 1803
1747 cctttaccttACGAGACGACCCCAACAGAGGACATGCGGAGTGTGGCCAAAGAAATTTGACATC 1806
1804 ccttccactcagaggaacccaagagcgagtgcggyggttggccaaggaattggacatc 1863
1807 TCGTGTGTCAAAATTTGACAGGTGATCGAGACGAGGGAGTTTGGCGAGGCTGTCAATGGC 1866
1864 tcgtgtgcaaatgtgacaggtgtatcggagcaaggygagtttgcgaggtctgcagtgyc 1923
1867 CACCTGAAGCTGCCAGGCAAGAGAGAGATCTTTGGCATCAAGACCTCAAGTCGAGGCG 1926
1924 cactgaagctgcccagtggaagagagatcttgtgtgccaacaaagctcaagtctgagc 1983
1927 TACAGGAGAAAGCAGCGCGGACTTCTTGAGCGAAGCCTCCATCATGAGCGAGTTGAGC 1986
1984 tacaggaagaagcagcgccgagcttcttgagcgagctccatcatgtgccaagtctgac 2043
1987 CATCCCAAGCTCATCCACTGAGGCTGTCTGACCAAGACGACACCTGTATGATCATC 2046
2044 catcccaagctcatccacttgaggtgtgtgtgaccaaagagacacgtgtatgatactc 2103
2047 ACCGAGTTTCATGAGATAGGCTCCTGTGACCTCTTTCGCGCAAAAGATGGAGATTTC 2106
2104 accgagtttcatggaagaaagtgcccttgactcttcttcgcgcaaaagatggygaagctc 2163
2107 ACAGTATCCAGCTGTGAGGATGCTTGCGGGCATGCGAGCTGCATGAATGACTGTGCA 2166
2164 acagtatccagctgtgtggaagcttctcggygcatcgaagctgtgatatgaactgtgca 2223
2167 GACATGAACTATGTTTACCGGTATCTGGCTGCCCAACATCCTGTGTAACGCAACCTG 2226
2224 gacatgaactatgtttacccgtgactgtgcgcgcaaatcttgcataacagcaacctg 2283
2227 GGTGTCAAGGTGTCGACTTGTGGCTTCACGCTTTCATGAGAGAGATACCTCAGACCC 2286
2284 ggtgtcaaggtgtcgtactgtgtgtctcacaagcttcttagaagaatacctcagaacccc 2343
2287 ACCTACACCAAGTCCCTGGGGGCAAAATTTCCCATTCGCTGTGACAGCCCGGAAACCATC 2346
2344 acctacaccaagtgcccttggygcgaagaatccccatctgcgtgacacgcccgyaagccatc 2403
2347 CAGTACCGGAAGTTCACTCGGCGCAAGTGATGTGAGACTGAGCATTTGCTATGTGGAG 2406
2404 cagtagtccctatgggagggcgccctacttgagacatgacacacagagatgtaatgagcc 2466
2407 GTGATGCTCTATGGGAGGCGGCTTACTGAGACATGACCAACAGAGATGTAATCAATGCC 2466
2464 gtgagtctctatggygaggygcctactgtggaatgacacacagatgttaatcaatgccc 2523
2467 ATTGACGAGACTATCGCTGCCACCGCCATGAGACTGCCCGCAGCGCCTGTGACCAATC 2526
2524 attgagcagactatcgtgtgcacgcgcccacgtactgcccagctgtcctgtgacaactc 2583
2527 ATGCTGGAGTGTGGTAGAAGACCGCAACACCGGCCCAAGTGGGCCCAATTTGCAAC 2586
2584 atgctggagtgttggtagaagacgccaacacgcgcccagatctgccaatgttcaaac 2643
2587 ACGCTGACAAAGATGATCGCAATCCCAACAGCCTTCAAAGCCATGGCGCCCTCTCTCT 2646
2644 acgtgtaagaagatgtatccgcaatcccaacagctctcaagaacatgtgcccctctcctct 2703
2647 GGCATCAACCTGCGCTGTGTGACCGCACGATCCCGACTACCAACAGCTTTAAACAGG 2706
2704 ggcataacctgscgtgtgtgacccgcacgatccccgataacacagcttataacagtg 2763
2707 GACGATGGCTGAGGCGCATCAAGATGGGGGAGTCAAGAGAGCTTGGCCATGCGCGGC 2766
1687 gtgtgcatcgcatcgtgtgttaacagacggyggttggcgctgtcgtacgtgagtaacg 1743
1687 gacaagctgcaaaccttaacacagtggtcacatgacatgacccaagatgaatctacatcgat 1803
1747 cctttaccttACGAGACGACCCCAACAGAGGACATGCGGAGTGTGGCCAAAGAAATTTGACATC 1806
1804 ccttccactcagaggaacccaagagcgagtgcggyggttggccaaggaattggacatc 1863
1807 TCGTGTGTCAAAATTTGACAGGTGATCGAGACGAGGGAGTTTGGCGAGGCTGTCAATGGC 1866
1864 tcgtgtgcaaatgtgacaggtgtatcggagcaaggygagtttgcgaggtctgcagtgyc 1923
1867 CACCTGAAGCTGCCAGGCAAGAGAGAGATCTTTGGCATCAAGACCTCAAGTCGAGGCG 1926
1924 cactgaagctgcccagtggaagagagatcttgtgtgccaacaaagctcaagtctgagc 1983
1927 TACAGGAGAAAGCAGCGCGGACTTCTTGAGCGAAGCCTCCATCATGAGCGAGTTGAGC 1986
1984 tacaggaagaagcagcgccgagcttcttgagcgagctccatcatgtgccaagtctgac 2043
1987 CATCCCAAGCTCATCCACTGAGGCTGTCTGACCAAGACGACACCTGTATGATCATC 2046
2044 catcccaagctcatccacttgaggtgtgtgtgaccaaagagacacgtgtatgatactc 2103
2047 ACCGAGTTTCATGAGATAGGCTCCTGTGACCTCTTTCGCGCAAAAGATGGAGATTTC 2106
2104 accgagtttcatggaagaaagtgcccttgactcttcttcgcgcaaaagatggygaagctc 2163
2107 ACAGTATCCAGCTGTGAGGATGCTTGCGGGCATGCGAGCTGCATGAATGACTGTGCA 2166
2164 acagtatccagctgtgtggaagcttctcggygcatcgaagctgtgatatgaactgtgca 2223
2167 GACATGAACTATGTTTACCGGTATCTGGCTGCCCAACATCCTGTGTAACGCAACCTG 2226
2224 gacatgaactatgtttacccgtgactgtgcgcgcaaatcttgcataacagcaacctg 2283
2227 GGTGTCAAGGTGTCGACTTGTGGCTTCACGCTTTCATGAGAGAGATACCTCAGACCC 2286
2284 ggtgtcaaggtgtcgtactgtgtgtctcacaagcttcttagaagaatacctcagaacccc 2343
2287 ACCTACACCAAGTCCCTGGGGGCAAAATTTCCCATTCGCTGTGACAGCCCGGAAACCATC 2346
2344 acctacaccaagtgcccttggygcgaagaatccccatctgcgtgacacgcccgyaagccatc 2403
2347 CAGTACCGGAAGTTCACTCGGCGCAAGTGATGTGAGACTGAGCATTTGCTATGTGGAG 2406
2404 cagtagtccctatgggagggcgccctacttgagacatgacacacagagatgtaatgagcc 2466
2407 GTGATGCTCTATGGGAGGCGGCTTACTGAGACATGACCAACAGAGATGTAATCAATGCC 2466
2464 gtgagtctctatggygaggygcctactgtggaatgacacacagatgttaatcaatgccc 2523
2467 ATTGACGAGACTATCGCTGCCACCGCCATGAGACTGCCCGCAGCGCCTGTGACCAATC 2526
2524 attgagcagactatcgtgtgcacgcgcccacgtactgcccagctgtcctgtgacaactc 2583
2527 ATGCTGGAGTGTGGTAGAAGACCGCAACACCGGCCCAAGTGGGCCCAATTTGCAAC 2586
2584 atgctggagtgttggtagaagacgccaacacgcgcccagatctgccaatgttcaaac 2643
2587 ACGCTGACAAAGATGATCGCAATCCCAACAGCCTTCAAAGCCATGGCGCCCTCTCTCT 2646
2644 acgtgtaagaagatgtatccgcaatcccaacagctctcaagaacatgtgcccctctcctct 2703
2647 GGCATCAACCTGCGCTGTGTGACCGCACGATCCCGACTACCAACAGCTTTAAACAGG 2706
2704 ggcataacctgscgtgtgtgacccgcacgatccccgataacacagcttataacagtg 2763
2707 GACGATGGCTGAGGCGCATCAAGATGGGGGAGTCAAGAGAGCTTGGCCATGCGCGGC 2766
1687 gtgtgcatcgcatcgtgtgttaacagacggyggttggcgctgtcgtacgtgagtaacg 1743
1687 gacaagctgcaaaccttaacacagtggtcacatgacatgacccaagatgaatctacatcgat 1803
1747 cctttaccttACGAGACGACCCCAACAGAGGACATGCGGAGTGTGGCCAAAGAAATTTGACATC 1806
1804 ccttccactcagaggaacccaagagcgagtgcggyggttggccaaggaattggacatc 1863
1807 TCGTGTGTCAAAATTTGACAGGTGATCGAGACGAGGGAGTTTGGCGAGGCTGTCAATGGC 1866
1864 tcgtgtgcaaatgtgacaggtgtatcggagcaaggygagtttgcgaggtctgcagtgyc 1923
1867 CACCTGAAGCTGCCAGGCAAGAGAGAGATCTTTGGCATCAAGACCTCAAGTCGAGGCG 1926
1924 cactgaagctgcccagtggaagagagatcttgtgtgccaacaaagctcaagtctgagc 1983
1927 TACAGGAGAAAGCAGCGCGGACTTCTTGAGCGAAGCCTCCATCATGAGCGAGTTGAGC 1986
1984 tacaggaagaagcagcgccgagcttcttgagcgagctccatcatgtgccaagtctgac 2043
1987 CATCCCAAGCTCATCCACTGAGGCTGTCTGACCAAGACGACACCTGTATGATCATC 2046
2044 catcccaagctcatccacttgaggtgtgtgtgaccaaagagacacgtgtatgatactc 2103
2047 ACCGAGTTTCATGAGATAGGCTCCTGTGACCTCTTTCGCGCAAAAGATGGAGATTTC 2106
2104 accgagtttcatg
```



|          |  |  |      |
|----------|--|--|------|
| Dd       | 2764   | gacgaagtcgtcgaaggccatcaagaatcggggcagtlacaagagagaagcttgcgaatgccgc | 2823 |
| Oy       | 2767   | TTCACTTCCTTGAACGTCGTCTCAGATGATGATGAGACATTCTCCGGGTTGGGGTC         | 2826 |
| Dd       | 2824   | ttcacctcccttgacgcgcgtctcatgatgatgagtagaacattctccgggttggggtc      | 2883 |
| Oy       | 2827   | ACTTTGGCTGGCCACACAGAAAAAATCTTGAAACAGTATCCAGGTATCGGGCCAGATG       | 2886 |
| Dd       | 2884   | aacttgcgtcgaccacagaaaaaaatccctgaacagatctcagtgatbcggcgcaagt       | 2943 |
| Oy       | 2887   | AACGAGATTACGTCTGGGSGGTTTACAATTGCACCTGCCCTCACCTTCTCTCCA           | 2946 |
| Dd       | 2944   | aaccagatctcagctctcgagggtttgacatlcacctgcctcgctcaccttctctcaa       | 3003 |
| Oy       | 2947   | GCCCCGCCCTCTGCG 2962   |      |
| Dd       | 3004   | gccccgccccctctgc 3019  |      |
| <br>     |  |  |      |
| RESULT   | 4  |  |      |
| AAA88549 |  |  |      |
| ID       | AAA88549   | standard; cDNA; 3949 BP.   |      |
| XX       |  |  |      |
| XX       | AAA88549;  |  |      |
| XX       |  |  |      |
| DT       | 22-JAN-2001  | (first entry)  |      |
| XX       |  |  |      |
| DE       | Human CASB616 cDNA.  |  |      |
| KW       | CASB616; EPHB2; ERK; EPH3; EPH3J; DRT; HEK5; EPHB2V;                 |  |      |
| KW       | receptor protein tyrosine kinase; human; antigen; colon cancer;      |  |      |
| KW       | ovary cancer; tumour; autoimmune disease; vaccine; gene therapy;     |  |      |
| KW       | diagnosis; ss.   |  |      |
| XX       |  |  |      |
| OS       | Homo sapiens.  |  |      |
| XX       |  |  |      |
| FH       | Key  | Location/Qualifiers  |      |
| FT       | CDS  | 26..3193   |      |
| FT       |  | /*tag= a   |      |
| XX       |  |  |      |
| PN       | WO200053216-A2.  |  |      |
| PD       | 14-SEP-2000.   |  |      |
| XX       |  |  |      |
| PF       | 28-FEB-2000; 2000MO-EP01587.   |  |      |
| XX       |  |  |      |
| PR       | 05-MAR-1999; 99GB-0005124.   |  |      |
| XX       |  |  |      |
| PA       | (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.                              |  |      |
| P1       | Vlnals De Bascols YC:  |  |      |
| XX       |  |  |      |
| DR       | WP1; 2000-587384/55.   |  |      |
| XX       | P-PSDB; AAB19591.  |  |      |
| XX       |  |  |      |
| PT       | Vaccine composition for treating ovarian and colon cancer, comprises |  |      |
| PT       | CASB616 polypeptides, polynucleotides or antigen presenting cells    |  |      |
| PT       | expressing the polypeptides -  |  |      |
| XX       |  |  |      |
| PS       | Claim 3; Page 41-42; 57pp; English.                                  |  |      |
| XX       |  |  |      |
| CC       | The present sequence is that of cDNA coding for human CASB616 (see   |  |      |
| CC       | AAB19591), a member of the EPH and EPH-related family of receptor    |  |      |
| CC       | protein tyrosine kinases. CASB616 is also known as EPHB2, ERK,       |  |      |
| CC       | EPH3, EPH3J, DRT, HEK5 and EPHB2V. CASB616 polypeptides and          |  |      |
| CC       | polynucleotides are important immunogens for specific prophylactic   |  |      |
| CC       | or therapeutic immunization against tumours, especially colon        |  |      |
| CC       | cancer (claimed) and ovarian cancer. They are specifically           |  |      |
| CC       | expressed or highly over-expressed in tumours compared to normal     |  |      |
| CC       | cells and can thus be targeted by antigen-specific immune            |  |      |
| CC       | mechanisms leading to destruction of the tumour cells. They can      |  |      |
| CC       | also be used to diagnose the occurrence of tumour cells. Their       |  |      |
| CC       | inappropriate expression can also cause an induction of autoimmune   |  |      |

CC responses, which can be corrected through vaccination using the  
CC CASB616 polypeptides or polynucleotides.  
XX  
SQ Sequence 3949 BP; 934 A; 1142 C; 1105 G; 768 T; 0 other;

|                       |              |              |               |              |
|-----------------------|--------------|--------------|---------------|--------------|
| Query Match           | 97.4%        | Score 2884;  | DB 21;        | Length 3949; |
| Best Local Similarity | 99.6%        | Pred. No. 0; |               |              |
| Matches 2903;         | Conservative | 0;           | Mismatches 5; | Indels 6;    |
|                       |              |              |               | Gaps 1       |

|    |     |  |      |
|----|-----|--|------|
| QY | 1   | CTGTCTCGCCGCGCTGGGAAGAAAGCTTAATATGACTTCACATACAGCAGCTGCTAGCTGGGC    | 60   |
| Dp | 68  | ctgtctcgcgcgcttggaaagaaacgcttaatgtaactccaatacgaactgtcttagcttggcc   | 127  |
| OY | 61  | TGGAATGGAGATCCCTCCATATGAGGTGGGAAGAGTGAAGGGGTACGATGAGAAACATGTAAAC   | 120  |
| Dp | 128 | tggaatggagatccctccatattgaggtggaaagagtgaagggtacgattcgaatacgtgaac    | 187  |
| OY | 121 | ACGATTCGCGACAGTACACAGGTGTCAACAGTGTATTGATTCAGCCAGACAGAACTGGCTACAGC  | 180  |
| Dp | 188 | acgattcgcgacagtacccaagctgtgcaagctgtgtgagtcgaagccagaagaaacacgtgtaag | 247  |
| OY | 181 | ACCAAGTTTATTCGGCGCCGCTGGGGCCCGACCGCATCCACGTGAGATGAATTTTCGGTG       | 240  |
| Dp | 248 | accaagttattccgcgcgttggccccaacgcatccaacgttgagatgtaagtttccgtg        | 307  |
| OY | 241 | CGTACATCGACGACATCCCGACGGTGGCGTCTCGTAAGAGAGACCTTCAACCTTAT           | 300  |
| Dp | 308 | cgtacatcgacgacatcccgacgggtggcgctctcgtaagagagacctccaacctcat         | 367  |
| OY | 301 | TACATATAGAGCTGACTTTGACTGAGCCACACAAACCTTCCCGACATGATGAGAGAAATCA      | 360  |
| Dp | 368 | tacatitagagctgacttgcgtctgcgcacaagaaccttcccaacctggaatgagaatcca      | 427  |
| OY | 361 | TGGGTGAAGGTGCATACCATTTGCAAGCCGACGAGAGACTTCTCCAGGTGAGACTGGGTGC      | 420  |
| Dp | 428 | tgggtgaaggctgataccattgacgcggaagagcttctcccaagtggaaccttggctg         | 487  |
| OY | 421 | CGCGTCATGAAATATCAACACCGAGGGGAGGTTTGGAACGTGTGTCGGCGAGCGGGCTTC       | 480  |
| Dp | 488 | cgcgctcatgaaatacaacacacgaagctggcgaagcttcggaacctggtccgcgaagcgtctc   | 547  |
| OY | 481 | TACCTGGCTCTTCAGAGACTATTTGGCGGCTCATGTCCCTCATCGCCGTGGCTTCTTTCAC      | 540  |
| Dp | 548 | tacctggctcttcgaagactatgvcggtcgtacatgtccctcatgcgcgtgtgtctctaac      | 607  |
| OY | 541 | CGCAAGTCCCGCCGATCATTCACGAATGGCGCCATTTCCAGAGAAACCTGTGGGGGCT         | 600  |
| Dp | 608 | cgcgaagtcccgccgatactacgaatgvgcactcttcagaagaaacctgtcggggct          | 667  |
| OY | 601 | GAGAGCACAATCCGTGGTGGGTGGCCGGGCGAGCTGATGGCCAAATGCGAAGAGTGGAT        | 660  |
| Dp | 668 | gagagcacaatccgtgggtgggtggccgggacgtgatggccaaatgcgaaagatgtagat       | 727  |
| OY | 661 | GTACCCATCAAGGCTTCTACTGTAAAGGGGAGAGGGGAATGGCTGGTCCCATCGGCGCTGC      | 720  |
| Dp | 728 | gtaccacataagctctactactgtaaacgggagagcgagctgtgtgtgcatacgggcgtgc      | 787  |
| OY | 721 | ATGTGCAAGACGAGGCTTTCGAGGCCGTTTGAAGATGCAACCGTGTGCCGAGGTTCATCT       | 780  |
| Dp | 788 | atgtgcaagacgagctctgcggccgtttggaatgtaacacgctctgcgaggtgtgtccactt     | 847  |
| OY | 781 | GGGAGCTTCAAGGCGCAACCAAGGGGATGAGGGCTGTACCCATATGTCATCAACAGCCGG       | 840  |
| Dp | 848 | gggagcttcaaggcgcaaccaaagggaatggagctgttaaccaatgttccaataaagccgg      | 907  |
| OY | 841 | ACCACTTCTAAAGGGGACACCAACTTGTCTCGCGCAATAGGTACTTACAGAGACACCTG        | 900  |
| Dp | 908 | accacttctgaagggtgcacaacactgtgtctgcggaatggtactatacgaagcagaacctg     | 967  |
| OY | 901 | GACCCCTGGACATGCCCTTCACACCAACATCCCTCCGGCGCCCGACGCTGTGATTTCCAGT      | 960  |
| Dp | 968 | gaccccttgaaatgtcccttcaacaacaatccctctgcgcccgaagctgtgttctcaagt       | 1027 |



[illegible]

|           |  |  |      |
|-----------|--|--|------|
| QY        | 2035   | GTGATGATCATCATCCAGAGTTCTATGAGAGATAGGCTCCCTGGAGATCTCTTCTCCGGCAAAAC    | 2034 |
| Db        | 2108   | gtgatgatacatcacaccagagttctatgagagaatgagctccctggagatctcttctccggcaaaac | 2167 |
| QY        | 2095   | GATGGGCGGTTCCACAATCATCCAGCTGNTGGGATGCTCTGGGGCATCGACCTGGCATG          | 2154 |
| Db        | 2168   | gatgggcagttccacaatcatccagctgntgggagtgctctggggcattcgacctggcatg        | 2227 |
| QY        | 2155   | AAGTACCTGGCAGACATGAACATATGTTACACCGTGACCTGAGCTGACCCGCAACATCTCTGTC     | 2214 |
| Db        | 2228   | aagtaacctggcagacatgaaatattgtttacacgtgacctgagctgaccccgcaacctctctgc    | 2287 |
| QY        | 2215   | AACGACAACTCGTGCTGTGCAGAGGTGTGAGATTTTGGGCTCTCACGCTTCTTAAAGAGCAT       | 2274 |
| Db        | 2288   | aacgacaacctcgtgctgtgcagaggtgtgagattttgggctcttcacgcttcttaagagacgat    | 2347 |
| QY        | 2275   | ACCTAGACCCCCACCTCTACACAGAGCCCTGGGGGAAAGTTGCCCATCCGCTGGACACACC        | 2334 |
| Db        | 2348   | acctagacccccacctctacacagagccctgggggaaagtggcccatccgctggacacacc        | 2407 |
| QY        | 2335   | CCGGAAGCCATTCAGATACCGGAAGTTTACCTCGGCCAGTGTGTGTGAGCTTACGGCATT         | 2394 |
| Db        | 2408   | cchggaagccatttcagataccggaaagttttacctcgggccagtgtgtgtgagctttacggcatt   | 2467 |
| QY        | 2395   | GTCATGTGGGAGGTCGATGTCTCTATGGGGAGACGGCCCTACTGTGGACATGACCAACCAAGAT     | 2454 |
| Db        | 2468   | gtcatgtgggaggtcgaatgtctctatggggagacggccctactgtggacatgaccaaccaaagt    | 2527 |
| QY        | 2455   | GTAAATCAATGGCATTTTATGACAGAGATATCGGCTGCTCCACCGCCATGGAGCTGCCGAGACC     | 2514 |
| Db        | 2528   | gtaaatcaatggcattttatgacagagatatcggctgctccacggccatggagctgcccgagacc    | 2587 |
| QY        | 2515   | CTGCACCAACTCATGTGTGAGATGTTTGGCAGAGAAGACCGCAACCCAGCGCCAAATTGSGC       | 2574 |
| Db        | 2588   | ctgcaccaactcatgtgtgagatgtttggcagagaaagaccgcaacccagcgccaaattgsgc      | 2647 |
| QY        | 2575   | CAAAATTGTCAACACAGCTTAGACAGATGATCCGAATCCCAACAGCTTCAAACCATTTGGCG       | 2634 |
| Db        | 2648   | caaaattgtcaaacacagcttagacagatgatccgaatcccaacagcttcaaagccaatggcg      | 2707 |
| QY        | 2635   | CGCCCTCCTCTGGCATTCAACCTGCGCGCTCTGGACCGGACGATCCCGCAGTACACACAGC        | 2694 |
| Db        | 2708   | ccgccctcctctggcatttcaacctgcgcgctctggacgggacgatcccgcatcacaccagc       | 2767 |
| QY        | 2695   | TTTAAACAGGTCGAGCAGATGGCTGAGAGCCATAGATGGCGCAGTACAGAGAGAGCTTC          | 2754 |
| Db        | 2768   | tttaaacaggctcagcagatggctgagagccatagatggcgcatgacagagagcttc            | 2827 |
| QY        | 2755   | GCCAAATGCCGGCTTCCACTCTTTGACGTCGTGTCTCAGATGATGATGAGAGCAATTCTC         | 2814 |
| Db        | 2828   | gccaaatgccggcttccactctttgacgtcgtgtctcagatgatgatgagagcaattctc         | 2887 |
| QY        | 2815   | CGGGTTGGGGGTCACCTTTGGGTCGGCGCACCAAAAAATCCTGAACAGTATCCAGGTGATG        | 2874 |
| Db        | 2888   | cgggttgggggtcacctttgggctcggcgcacaaaaaatcctgaacagtattccaggtgatg       | 2947 |
| QY        | 2875   | CGGGCGAGATGAACACAGATTCACTGTGTGAGAG 2908                              |      |
| Db        | 2948   | cgggcgagatgaacacagatttcaactgtgtgagag 2981                            |      |
| RESULT    | 5  |  |      |
| AAAT84528 |  |  |      |
| ID        | AAAT84528  | standard; cdna; 3105 bp.   |      |
| XX        | AAAT84528;   |  |      |
| AC        |  |  |      |
| XX        |  |  |      |
| XX        |  |  |      |
| DT        | 02-DEC-1997  | (first entry)  |      |
| XX        |  |  |      |
| DE        | Mouse Nuk  | tyrosine kinase cdna.  |      |
| XX        |  |  |      |
| KW        | Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction; axonogenesis; neurodegenerative disease. |  |      |

[illegible]

|    |      |  |      |
|----|------|--|------|
| Db | 127  | tggatggtatacattccccaatcaaggctgggaagaagtgtagcggtctacgaacgaacatgaaac | 186  |
| Qy | 121  | ACGATCCGACGACTACGAGGTGTGCAACCTGTGTTGAGTCAACCCAGAACACTGGTACGG       | 180  |
| Db | 187  | actatcgttaacctataccaggctgtagaaigtctcttgtagtaagccgaacaaactgctgcg    | 246  |
| Qy | 181  | ACCAATTTTATCCGGCGCCGTGGGGCCCAACCGCATCCACGTGGAGATGAAGTTTTCGGT       | 240  |
| Db | 247  | accaaattatccctcggcgctggcgcccaacgtaatacagctgtagaagaaagattctcgtg     | 306  |
| Qy | 241  | CGGATGTGACGAGATCCCGACGCTGGCTGGTCTGCTGCAAGAGACTTTCACCTCTAT          | 300  |
| Db | 307  | cgtgactgtcagaagaatctcccaagctgctgcgggtctcccgaaagagactctcaacctaa     | 366  |
| Qy | 301  | TACTATGAGCGCTGACTTTGACTCTGGCCACCAAGACTTTCCCACTGGATGAGAAATCCA       | 360  |
| Db | 367  | tactatgaagcctgtaatttgacttaagcccaaaaactcttcccaactgatactgaaatccg     | 426  |
| Qy | 361  | TGGGTAAAGTGGATACCATTTGACCCGACGAGAGCTTTCGCCAGTGGAGACTGGGTGGC        | 420  |
| Db | 427  | tgggtgaagtgtagaaccaatcgcgggcgaatgaagactctctcccggtggaaccgggtgcg     | 486  |
| Qy | 421  | CGGCTATGAANAATCAACACCGAGGTGGCGAGCTTTCGACCTGTGTTCCGACGGCTTC         | 480  |
| Db | 487  | cggctatgaataatacaacatgtaggtgtgaaagctcgtgtctgtgtccgcaatgtttc        | 546  |
| Qy | 481  | TACCTGGCTTTCAGAGACTATTTGGCGGCTGCAATGTCCCTCATCCGCGTGCCTCTTAC        | 540  |
| Db | 547  | tacctggcttccaaagactaaagctagcggtctgtatgtctctcatctgtctgcgctcttac     | 606  |
| Qy | 541  | CGCAAGTGGCCCGGCATCATCCAGAAATGGCCCAATCTTCCAGAGAAACCCGTGGGGGT        | 600  |
| Db | 607  | cggaaagtccccgaatacatacgaatgtgtgcaatctctccagaagacatactcgggtgtc      | 666  |
| Qy | 601  | GAGAGACATCGCTGTGTGGTGTCCCGGGGACGCTGCATCCCCAAATCGGAGAGGTGAT         | 660  |
| Db | 667  | gagagcaactctgctgtgtgcagctcgggcagctgtcaatcgcaatgctgaagatgtagac      | 726  |
| Qy | 661  | GTACCCATCAACCTTACTGTAAAGGGGAGCGGAGTGGTGGCCATTCGGGGGCTGC            | 720  |
| Db | 727  | gtgccatacaaatcttactctgtataaaggggaacggcgaatgtgtgtgtccatcgtgtcgtc    | 786  |
| Qy | 721  | ATGTCAAGACGAGCTTTCGAGCGCGTTTGAGAGATGGCACCGCTGTCCGAGGTGTCCATCT      | 780  |
| Db | 787  | atgttcaagggcgggtctcgaagctgtgtgagaacggcaacgctctgcggaagttgtccatca    | 846  |
| Qy | 781  | GGGACTTTCAGAGGCCAACAGAGGGGATGAGAGGCTGTACCCACTGTCCCAATCAACAGCCG     | 840  |
| Db | 847  | ggaacctcaagggcaacaaagggaagcaagcctgtgcacccaactccatcaaacagcgctc      | 906  |
| Qy | 841  | ACCATTCTGAAGGGGCCACCAACTGTGTGTGGCGCAATGGCTACTATACAGACAGACTG        | 900  |
| Db | 907  | accacctctggagtggtgcacaaactgtgtatgtgcgaaacggtctactataagggcgcaactc   | 966  |
| Qy | 901  | GACCCCGGACAAATGGCCCTGTGACAAACAATCCCTCCGCGCCCAAGGCTGTGATTTCAGT      | 960  |
| Db | 967  | gaacctctagaacatgacctgtgacaaccaataccctctgtgcgcccaaggtctgtactccagc   | 1026 |
| Qy | 961  | GTCAATGAGACTCCCTCATGCTTGAATGGAACCCCTCCCGGCACATCCGGAAGCGGAGAG       | 1020 |
| Db | 1027 | gtcaacgagacatacctcatatgtctatgagtgtgaacccaaccccgagatctcgggtgtcgcgag | 1086 |
| Qy | 1021 | GACTCTGCTTCAACATCATCTGTGCAGAGCTGTGGCTCGGGCCGGGCTGCTGCACCCGC        | 1080 |
| Db | 1087 | gactctgtttacaacatacatctcgaagagctgtgtctcgcgcgggtgcgctgtgcacgcgc     | 1146 |
| Qy | 1081 | TGGCGGACATGTACAGTACGACCAACGCGACACTTGGGCTGTACCGAGCAACGCAATTAC       | 1140 |
| Db | 1147 | tgcgggtgaacaagctgtcagtaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcac    | 1206 |
| Qy | 1141 | ATCAGTGACTGTGTCGCCACACACCCAGTACACTTGTGAGATCCAGACTGTGAACGGCTTT      | 1200 |
| Db | 1207 | atcagtgacctgtcgtggaacacacgaatgaacactctgtgagatacgaacgctgaatgattta   | 1266 |

1201 ACTGACGAGCCCTTCTGCTCAGTTGGCTCTGTGAATCATCAACCAACGACGCA 1260  
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 1327 gacacatcgccggtgctcctcctcagctcagctcgtcgtgaaatcaacacacaa 1386  
 1321 TCGTGGTCCACGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCG 1380  
 1387 tctgtctccacgacgac 1446  
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 1855 GTTTCGACGTGGCACTGAAAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1914  
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 1915 CTCAAGTCGGGCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1974  
 1987 ctcaagtcagagatcag 2046  
 1975 GGGCAGTTGCGACATCCCAAGTCATCCACCTGAGGAGGAGTCTGTGACCAAGAGCA 2034  
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 2215 AACGACAACTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2274  
 2287 aacagtaactggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2346

2275 ACCTCAGACCCACCCACACACAGTGCCTGGGCGGAGGAGGAGGAGGAGGAGGAGGAG 2334  
 2347 acgttgaccccccac 2406  
 2335 CCGGAGCCATTCACGATACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2394  
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 2395 GTGATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2454  
 2467 gtaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2526  
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 2527 gtaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2586  
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 2587 ctgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2646  
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 2767 ttaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2826  
 2755 GCGAATGCGGCTTACCTCTTACGCTGTGATGATGATGATGATGATGATGATGATGATGAT 2814  
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 2875 CCGGCGCAGATGACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2934  
 2947 cgggcccagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3006  
 2935 CTCTTCTCTCAAGCCCGGCC 2954  
 3007 cctctctcctcagcgccccc 3026

RESULT 6  
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 ID AAT07308 standard; cDNA; 3105 BP.  
 XX  
 AC AAT07308;  
 XX  
 DT 19-MAR-1996 (first entry)  
 XX  
 DE Receptor tyrosine kinase (neural kinase) cDNA.  
 XX  
 KW Receptor tyrosine kinase; neural kinase; Nuk gene; axon;  
 KW axonogenesis; nerve disorder; gene therapy; transgenic animal; ss.  
 OS Mus musculus.  
 OS  
 XX  
 XX  
 FH Key  
 FT CDS 1..2985 Location/Qualifiers  
 FT 1..78 /tag= a  
 FT sig\_peptide  
 FT 79..2982 /tag= b  
 FT mat\_peptide  
 FT /tag= c  
 XX  
 PN M09530326-A1.





QY 61 TGGATGTCATCTCTCATCAGGGTGGAGAGGTGAGTGGCTTACCATGAGAACAATGAAAC 120  
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Db 136 Tggatggtgcacatcctccctcaggtgaggaaagtgagtgataagatgagaacaatgaaac 195  
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QY 121 AGGATCCCGACAGTACGAGTGTGCAACGTGTTGATGCAAGCCAGAAACAATGGCTACGG 180  
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Db 196 accatccgacattaccagatgtgcaagctcttgaaatcccaagccaataaactggtcgtcg 255  
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QY 181 ACCAAGTTTATCCGGCCGCGTGGGCCACCGCATCCAGTGGAGATGAAGTATTTTCGGT 240  
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Db 256 accaagatcaccagaggtcgagagcgacatccacgtgaggaatgaaatcttcgcgt 315  
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QY 241 GGTGACTGACAGATATCCCAAGGTGCTGCTCTGCAAGAGAACCTTCAACCTCTAT 300  
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QY 361 TGGTGAAAGTGTGATPACCATTTGCAAGCCGACGAGACTTCTCCAGTGGACCTGGTGGC 420  
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QY 421 CGCGTCAATGAATAATCAACACCGAGGTGGAGCTTCCGACTGTGTCCCGACGCGCTTC 480  
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Db 496 cgggtgtatgaatlaaacaacgaagtgccgaagcttctgagctctctcctcaaaaacgtctc 555  
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QY 481 TACCTGGCTTCAGAGACTATGGCGGTGCATGTCTCATCGCGCTGCGCTTCTTAC 540  
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Db 616 cgaagatgctcccgctgtaatacgaacggtggtctctccagaaacccctcgtggagcg 675  
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QY 601 GAGAGCATATCGTGTGGTGGCCCGGGGAGCTGCATCCCATGCGGAAGAGTGGAT 660  
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Db 676 gagagacacatctctgtgtgcaagccggggagacgtgcaatcgaatgagagaggtgagat 735  
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Db 1036 gtgaaatgaataccctctgt 1095  
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QY 1021 GACCTGTCTACAAATCATCTGCAAGAGCTGTGCTCGGCGCGGGGTCTCTGACCCCGC 1080  
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Db 1096 gactcgtgtatatacaatactctcgaagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1155  
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Db 1156 tgt 1215  
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QY 1141 ATCAGTACCTGCTGTGGCCACACCCAGTACACTTCGATTCAGAGCTGTGAACGGGGTT 1200  
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Db 1936 gaggt 1995  
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Db      2296 gtcaacagcaaccctgctcgaaggtgctcgaacttcgcccctccctcctcctgtagagat 2355
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Oy      2332 GCGCCGGAAGCCATCCAGTACCGGAAGTTACCTCGGCCAGTGTGTGAGCTACCGC 2391
Db      2416 ggcctctggagcaatcagctacgaaatcacaacagcagcagatgltgtagctatgga 2475
Oy      2392 ATTGTCAATGTGGAGAGTATGTCTCATGTGGAGAGCGCCCTACTGAGACATACCAACAG 2451
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Oy      2512 GCGCTGCACCAACTCATCTGAGTCTGTTGGCAGAGAAGACCCACACCGGCCCAAGTTC 2571
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Db      2776 agcttcaaacatgtagatgaaatgctgagctgcaatcaagaatgagcagtagaagagagc 2835
Oy      2752 TTGCGCAATGCGCGCTTCACTCTCTTGTGACGTGTGTCTCAAGATGATGATGAGAGACAT 2811
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Oy      2812 CTCGCGGTTGGGCTCACTTTGGCTGGCCACGAGAAAATACTCAACGATTCAGAGTGT 2871
Db      2896 ctacagctggtggtctcatttagacagacacagaaagaaatcttgaacagctccaagtg 2955
Oy      2872 ATGCGGCGCAGATGAAACAGATTCAGTGTGTGAGAGTTTGAATTCACCTGCTCGGCT 2931
Db      2956 atgagagcacaagatgacaacaatcagctctgtgtaggtttgtagaacaacagctccgtg 3015
Oy      2932 CACCTCTCTCTCAAGCGCCGCCGCC 2957
Db      3016 ctccactcctctgagcgccctgctccc 3041

RESULT 8
AA090657
ID      AA090657 standard; DNA; 4097 BP.
XX
AC      AA090657;
XX
DT      11-NOV-1995 (first entry)
XX
DE      Eph-related PTK Cdk5+.
XX
KW      Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
XX      prognosis; ss.
XX
OS      Gallus sp.
XX
FH      Key Location/Qualifiers
FT      10..3045
FT      CDS /tag= a
XX
XX      MO9515375-A.
XX

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PD      08-JUN-1995.
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XX      07-SEP-1994; 94MO-US10140.
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XX      03-DEC-1993; 93US-0162809.
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XX      (LJOL-) LA JOLLA CANCER RES FOUND.
XX
XX      Pasquale EB, Sajjadi FG;
XX
XX      WPI; 1995-215256/28.
XX
XX      P-PSDB; AAR75709.
XX
XX      Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
XX      cancer.
XX
XX      Claim 2; Page 71-75; 129pp; English.
XX
XX      A cDNA clone encoding a novel variant of Eph-related PTK Cdk5,
XX      Cdk5+ (AA090657), was isolated from a chick embryo library in
XX      lambda gt11. Cdk5+ protein (AAR75709) contains a 16-amino acid
XX      insertion in the juxtamembrane domain, and be a result of
XX      alternative splicing. Cdk5+ is exclusively expressed in the CNS.
XX
XX      Sequence 4097 BP; 1014 A; 1029 C; 1087 G; 967 T; 0 other;
XX
Query Match 71.8%; Score 2127.6; DB 16; Length 4097;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 464; Indels 57; Gaps 3;
Oy      1 CTGCTCGCGCGGTGGAAGAAGCGTAAATGAGTTCACACTACAGCAGTCTGAGACTGGC 60
Db      76 ctgctcgcgcggtggaagagcgtatgagctcacaacagcagcagcagcagcagcagcagc 135
Oy      61 TGGATGTGTCATCTCTCCATTCAGGGTGGAGAGGAGTGTGCTGATGAGACATGAAC 120
Db      136 tggatgtgtcatctctccatctcagggaggagagagagagagagagagagagagagagagac 195
Oy      121 ACGATCCGACGATACAGAGTGTGCAACGTGTTGAGTCAGACGAGACACTGCTACGG 180
Db      136 acgatccgacgatatcagagtggtgcaacgtgttgagtcagacgagacactgctacgg 255
Oy      196 accatccgacactacagctgctgcaagctcttgatccagcacaacaaactgctgagc 240
Db      181 ACCAAGTTATCCGCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGAAATTTTGGTG 240
Oy      256 accaagttatccgcgcggtgggcccacccgacatccagtggaagagaaatctcgtt 315
Db      241 CGTGACTGAGCAGCAGTCCCGCAGCTGCTGAGCTCTCTCAAGAGACCTTCAACTTAT 300
Oy      316 cgtgactgagcagcagtcctccgagctgagctctctgtagagagactttaacctat 375
Db      301 TACTATGAGGCTGACTTGTACTGCGCCACAGACCTTCCCACTGATGAGAGATGCA 360
Oy      376 tactatgagactgacttgtactgcgccacagacacttctcctaactgagtagaataacct 435
Db      361 TGGGTGCAAGTGGATACCATGTCAGCCGAGAGACTTCTCCAGATGAGATGGGTGGC 420
Oy      436 tgggtgcaagtggataccatgtcagccgagagactctctcgagtgagacttggtgg 495
Db      421 CGCGTATGAATAATCAACACGAGGTGGAGACTTCGAACTGTGTCCCGCAGCGGCTTC 480
Oy      496 cggtgatagaataatacaacacgaggtggcagcttctgagcagctcgaataaaggttcc 555
Db      481 TACCTGGCTTCCAGACTATGAGCGCTGATGTCCTTCATGCGCGTGTCTTTCAC 540
Oy      556 tacctggcttccagactatgagcgctgagctgagcttctgagcagctcgaataaaggttcc 615
Db      541 CGCAATGCGCCCGCATATCCAGATGAGGCGCATCTTCAGAGAAACCTGTGCGGGGCT 600
Oy      616 cgcgaatgctcccgcatatccagatgagggcgcatcttcagagaaacctctcgaggagc 675
Db      601 GAGAGCACATGCTGTGCTGCTCCGCGGCGACCTGCATCGCCAAATGCGAAGAGGTGAT 660

```



Db 676 gaaagacaatctctggtgagccggggagatgcatcagcaatgctggaagatgagat 735  
Oy 661 gTACCATTCAACCTTACTGTATGAACGGGAGCGGAGTGGCTGGTCCATCGGGGCTGC 720  
Db 736 gtgcccataaagctgtaactgcaatgagatgagctggtggtccatctggccgctgc 795  
Oy 721 ATGTCAAAAGCGGTTTGAGAGCCCTTGAAGATGACACCGTCTGCCAGAGTTGTCAACT 780  
Db 736 atgtgcaagccgggtctatgagctggtgagaaatgagaccgtctgcaagagctgcacatca 855  
Oy 781 GGGACTTTCAAGGGCCAAACCAAGGAGTGAAGGCGCTTACCCACTGTCCATCAACAGCGG 840  
Db 856 gggaaecttcaagggccagcaaggaatgaaagatgctccatctgtccaaatcaacggccgg 915  
Oy 841 ACCACTTGTGAAGGGGCGACCAACTGTGTCTGCCAAATGGCTTACTACAGACAGACCTG 900  
Db 916 agaaecttcaagggccagcaagatgctggtgcaaaagatatataccgggcaagatgct 975  
Oy 901 GACCCCGTGAATGCCCTTGCACAAACCATCCCTTCGGCCCGCCAGGCTGTGATTTCCAGT 960  
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Oy 961 GTCAATGAGACCTCCCTCATGCTGTGAGTGAAGACCCCTCCCGGACCTCCGGAGCGGAG 1020  
Db 1036 gtgaatgaaactccctctgactgagatgagaccccaacacacacacacacacacacacac 1095  
Oy 1021 GACCTCGTCAACATCATGTGCAAGAGCTGTGGCTCGGGCGGGGTGCTGCACCCGC 1080  
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Oy 1081 TGGGGGCAATGTATAGTATAGGACACACCGCAAGCTTGCAGATCAGGCTGTAAAGGCGCT 1140  
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Oy 1141 ATCAGTGAACCTGTGGCCACACACAGTACACTTTCGAGATCAGGCTGTAAAGGCGCT 1200  
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Oy 1201 ACTAACCAGAGCCCTTCTGCGCTCAAGTTGCGCTGTGAAACATACACACACACAGCA 1260  
Db 1276 acgaacgaagccctctctccacacacacacacacacacacacacacacacacacacac 1335  
Oy 1261 GCTCATCGGAGTGTGCATCATGATCAGTGTAGCGGACCGGAGACAGCATTAACCTG 1320  
Db 1336 gtctcttcagcgctgtctcaataagcaacaggtcagcgcaactgtgcaagaatlaaccc 1395  
Oy 1321 TCGGTGTCCAGCGGAGACCCCAATGGCTGTGATCTGTGACTATGAGCTGCACTACTAT 1380  
Db 1396 tctgtgtctcaactgacgaaccccaatgagatctcctgtgatactgagctgcaatactat 1455  
Oy 1381 GAGAAGAGCTCACTGATGATCAACGCCCAAGCCCTAAAGCCCAACACAGGTCACG 1440  
Db 1456 gagaagaacactgagatgataatctcaacagcagtgaaagccccaacacacacactgtgaca 1515  
Oy 1441 G-----GCTCAAAAGCCGCGCCATCTATGTCTTCCAGGAGCGGAGACGACGTGTGGA 1494  
Db 1516 gtgcaaaaactcaaaagtctgcaacatcttaagtctccaaagtgtgagcaactacggtgct 1575  
Oy 1495 GGGTACGGGCGCTTACAGCGCAAGATGTACTTCCAGACATGACAGAAAGCCAGTACAG 1554  
Db 1576 gggatagccggtatagtgcaagatgtacttccagacacatgacatgaaagccgagctaacag 1635  
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Db 1756 gactctgagtaactctgcaagctgtgcaactataacagtggtgcaagctgactgacgtgtgt 1815

Oy 1718 -----TAAACCCAGGATGAGATGTACATC 1743  
Db 1816 ccccgccagcgctggt 1875  
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Db 1876 gatccatttaccatgaagaatcccaatgagctgtgcaagggaattctgcaaaagaatgtat 1935  
Oy 1804 ATTCCTGTGTCAAAATTTGACAGAGTGTATCGGACGAGGGAGTTTGGCGAGCTGTGCACT 1863  
Db 1936 atctctgtgtgaaatctgaacagatgtatgtgtgcaagggaggtgtgtgtgtgtgtgtgtgt 1995  
Oy 1864 GGCACCTGAAGCTGCCAGGAGAGAGATGTTTGTGGCCATCAACAGGCTCAAGCG 1923  
Db 1996 ggtgcatctcaagcttctctgtgcaaaagagatctctgtgtgtgtgtgtgtgtgtgtgtgtgt 2055  
Oy 1924 GGTACACGGAAGACAGCGCGGACTTCTGTAGCGAAGCCCTTCATCATAGGCGCAGTTTC 1983  
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Oy 1984 GACCATCCCAACGTCATCCACTTGAGAGGTGTGTCGACCAAGACACACCTGTGATATC 2043  
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Oy 2044 ATCACCGAGTTTCATGAGAAATGCTCCCTGGACTCTTTCGCGCAAAAGATGGGCGAG 2103  
Db 2176 attaacagaatctcaatgagaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2235  
Oy 2104 TTTCAGTCACTCAAGCTGTGTGGCATGCTTTCGAGGATCCGACGTGATGAATGACTG 2163  
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Oy 2164 GCAGACATGAACCTATGTTCACCGGTGACCTGGCTCCCGCAACATCTCTGTCAACAGCAAC 2223  
Db 2296 gctgatatgaactcaatgtgacacaggaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2355  
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Db 2356 ctgtctgcaaggt 2415  
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Db 2416 ccaacttacaacacagcgacacgt 2475  
Oy 2344 ATCCAGTACCGGAATGTACCTCGCGCAAGTGTGTGAGCTAAGGCAATTTGATATGTG 2403  
Db 2476 attcagtaacggaataatcacatacagccagcgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2535  
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Db 2536 gaagt 2595  
Oy 2464 GCCATTGACGAGACTTTCGGCTGCCACCGCCCATGAGACTGCCGAGCGCCCTGCACCAA 2523  
Db 2596 gctatgagagagacatctgt 2655  
Oy 2524 CTATGTGTGACTGTGTGGAGAGGAGCAGCAACACCGGCGCAAGTTTGGCCAAATTTGTC 2583  
Db 2656 ctatgtctgt 2715  
Oy 2584 AACACGTTAGACAAGATGATCCCAATCCACAGCCTCAAAAGCCATGCGGCCCTTCC 2643  
Db 2716 aaacactttagacaaaatgatacgaataatcccaatagatctgtgaagccatgtgcaactctctc 2775  
Oy 2644 TCTGGCATCAACCTGCGGCTGTGTGAGCGGACGATCCCGACTACACAGGCTTAAACAG 2703  
Db 2776 tctgt 2835  
Oy 2704 GTGAGCAGTGTGTGAGGCGCATCAAGATGTGGGAGTACAGAGAGAGCTTCCGCAATGCC 2763  
Db 2836 gtgtatgaaatgt 2895

|          |  |   |      |
|----------|--|---|------|
| YY       | 2764   | GGTTTCACCTCCTTTGAGCTGGTGTCTCAGATGATGAGACATTCCTCCGGTGGG            | 2823 |
| YY       | 2896   | 99cttcaccaccttgaatataatgatactcagaagactgtgagaacattctcaagattggg     | 2955 |
| OY       | 2824   | GTCACTTTGGCTGGCCACACGAAAAAAATCCTGAACAGATATCCAGGTGATGCGGGCGCAG     | 2883 |
| OY       | 2884   | ATGAACCAAGATTCACATCTGTGAGAGTTTGACATTTACCTCCGCTCCGCGCTCACCCTTTCCTC | 2943 |
| Db       | 3016   | atgaaccaaatctcagtcgtgaggttgatagcaacacgcttcctgctcattctcctt         | 3075 |
| OY       | 2944   | CAGGCCCGCCCGCC 2957   |      |
| OY       | 3076   | gagcgccctgctccc 3089  |      |
| Db       |  |   |      |
| RESULT   | 9  |   |      |
| AAO53471 |  |   |      |
| ID       | AAO53471   | standard; cDNA; 4281 BP.  |      |
| XX       | AAO53471;  |   |      |
| AC       |  |   |      |
| XX       | 16-JUN-1994  | (first entry)   |      |
| DT       |  |   |      |
| XX       | elk cDNA.  |   |      |
| DE       |  |   |      |
| KW       | lambda.gtl1; expression vector; lambda-BI-Elk; protein tyrosine kinase |   |      |
| KW       | Elk; BI; Eph; subfamily; receptor-like tyrosine kinase; eph; eck;      |   |      |
| KW       | phosphorylation; platelet-derived kinase insert domain; growth factor; |   |      |
| KM       | receptor kinase; platelet-derived growth factor receptor; ss.          |   |      |
| XX       |  |   |      |
| OS       | Rattus rattus.   |   |      |
| XX       |  |   |      |
| FH       | Key  | Location/Qualifiers   |      |
| FT       | CDS  | 367..3321   |      |
| FT       |  | /*tag= a  |      |
| FT       |  | /product= Elk   |      |
| XX       | CA2083521-A.   |   |      |
| PN       | 01-OCT-1993.   |   |      |
| PD       |  |   |      |
| XX       | 23-NOV-1992;   | 92CA-2083521.   |      |
| PF       |  |   |      |
| XX       | 31-MAR-1992;   | 92US-0861390.   |      |
| PR       |  |   |      |
| XX       | (MOUN ) MOUNT SINAI HOSPITAL CORP.                                     |   |      |
| PA       |  |   |      |
| XX       | Letwin K, Pawson A, Reedijk M;   |   |      |
| PI       |  |   |      |
| XX       | WPI; 1993-406300/51.   |   |      |
| DR       | P-PSDB; AAR44513.  |   |      |
| XX       |  |   |      |
| PT       | Expression of phosphorylated exogenous protein - in host cells         |   |      |
| PT       | transformed with two vectors, one for the protein, the other for       |   |      |
| PT       | catalytic domain of protein kinase                                     |   |      |
| XX       |  |   |      |
| PS       | Disclosure; Fig 3; 55pp; English.                                      |   |      |
| XX       |  |   |      |
| XX       | This sequence represents the elk cDNA which encodes the protein        |   |      |
| CC       | tyrosine kinase, Elk. The Elk gene, BI, encode a protein which is      |   |      |
| CC       | a member of the Eph subfamily of protein tyrosine kinases. The Elk     |   |      |
| CC       | product is very similar to two other receptor-like tyrosine kinases,   |   |      |
| CC       | eph and eck. Lambda-BI-Elk may be used in the production of            |   |      |
| CC       | phosphorylated exogenous protein along with a further vector encoding  |   |      |
| CC       | the desired exogenous protein. These plasmid may be used to produce    |   |      |
| CC       | phosphorylated proteins in host cells which have no intrinsic capacity |   |      |
| CC       | for phosphorylation, eg. bacteria. The system may be used for the      |   |      |
| CC       | expression of the phosphorylated kinase insert domain of a growth      |   |      |
| CC       | factor receptor kinase eg. platelet-derived growth factor receptor.    |   |      |
| XX       |  |   |      |
| XX       | Sequence 4281 BP; 1075 A; 1170 C; 1121 G; 915 T; 0 other;              |   |      |

| Query Match  | Similarity   | 55.1%   | Score 16.31    | DB 14  | Length 4281 |
|--------------|--------------|---|----------------|--------|-------------|
| Best Local   | Similarity   | 73.0%   | Pred. No. 0    |        |             |
| Matches 2128 | Conservative | 0   | Mismatches 780 | Indels | Gaps        |
| QY           | 5            | TCGCGCCGCTGGAGAAACGGCTAATGACATCCACTACAGCAGCTCTGAGCTGGCTGGA        | 64             |        |             |
|              |              |   |                |        |             |
| Db           | 410          | tgycgcgcatggaagaacatctgatagcacaaagaactgcaccttcagaagtctggaatgga    | 469            |        |             |
| QY           | 65           | TGGTGACATCCCTCCATCCAGGCTGGGAAGAGGTGAGTGGCTAGCATGAGAAACATGAAACACA  | 124            |        |             |
|              |              |   |                |        |             |
| Db           | 470          | cggccaaccctgcctctggtggtggaagaagtcagtggtctacgaatgaaaacctggaacca    | 529            |        |             |
| QY           | 125          | TCCGCACGTACCAAGGTGTGCAACAGTGTTCGATCAAGCCAGAACACTGGCTACGACCA       | 184            |        |             |
|              |              |   |                |        |             |
| Db           | 530          | tcctgacttaccgaatgctgcaacgctcttgaaccacacagaacaactgctgtaccaca       | 589            |        |             |
| QY           | 185          | AGTTTATCCGGCGCCCTGTGGGCCCCACCCGATCCACAGTGGAGATGAAAGTTTGGGTGGCGT   | 244            |        |             |
|              |              |   |                |        |             |
| Db           | 590          | ccattatcacagaagcggccccaatgcattctatcacagaatgtgcttccactctggaagg     | 649            |        |             |
| QY           | 245          | ACTGACGACGATCCGCCAGCGCTGTGGCTCTGCAAGAGACCTTCAACTCTATTACT          | 304            |        |             |
|              |              |   |                |        |             |
| Db           | 650          | actgaaagacgcttccaaatgtcccaagctcctctgcaagaagaccttcaactatactact     | 709            |        |             |
| QY           | 305          | ATGAGGCTGACTTTGACTCGGCGACCAAGCCTTCCCACTGGATGAGAAATCCATTGGG        | 364            |        |             |
|              |              |   |                |        |             |
| Db           | 710          | atgagactgactctgtcatgtccacaagaagaatcacgcttctgtgtctgtaagcccttacc    | 769            |        |             |
| QY           | 365          | TGAAGTGGATTCATTCGACCGCGAGAGAGCTTCGCCAGGTGACCTGGTGGCGCGG           | 424            |        |             |
|              |              |   |                |        |             |
| Db           | 770          | tcaagatgtgaaccacatctgtccagatgaaagcttctccagatgtgaatttgggggaagtg    | 829            |        |             |
| QY           | 425          | TCATGAAATCAACACCGAGGTGCGAGCTTTCGGACCTGTGTCCGACGCGCTTCTACC         | 484            |        |             |
|              |              |   |                |        |             |
| Db           | 830          | tgtatgaagtgaacaacagagaagtcagagaagctttggcgcttctaagaagtgttlltacc    | 889            |        |             |
| QY           | 485          | TGGCCTTCAGACATATGCGGCTGCTATCTCCCTCATCCGCCGTGGCTGTCTTACCGCA        | 544            |        |             |
|              |              |   |                |        |             |
| Db           | 890          | tcgcttccagatattatgtagcctgtatgtcttctacttctgtcgtgcttcttcaaaa        | 949            |        |             |
| QY           | 545          | AGTGGCCCCGCTACTTCCGAGATGGCGGCATGTTCAGAGAAACCTGTGGGGGCTGAGA        | 604            |        |             |
|              |              |   |                |        |             |
| Db           | 950          | agtgccccagcattgtgcaaaatttgcacgtgttccacagaacatgacagsgacagaga       | 1009           |        |             |
| QY           | 605          | GCACATCGCTGTGCTCGCCCGGCGGACGTGCATCGCCATCGGAGAGAGTGGATGTAC         | 664            |        |             |
|              |              |   |                |        |             |
| Db           | 1010         | gacactctctgtgtgtgtctggtcggtgacatgcatcccttaatcagaagaagtgtgaatgtgc  | 1069           |        |             |
| QY           | 665          | CCATCAAGCTACACTGTAACGGGGAGCGGGAGTGGTGGGCCATTCGGGCGCTGCATGT        | 724            |        |             |
|              |              |   |                |        |             |
| Db           | 1070         | ccataaactctactgcaatggaatggaagaaagtgtgtgtgtccatttgggcgtctgaacct    | 1129           |        |             |
| QY           | 725          | GCAAAAGCAAGCTTCCAGGCGCTGTGAGAAATGGCACCGCTGTCCGAGGTTGCTCATCTGGGA   | 784            |        |             |
|              |              |   |                |        |             |
| Db           | 1130         | gtaaggtgtgtcatgaacc--tgagaacagcgttgcctgcaagcgtctgtcgtcgga         | 1186           |        |             |
| QY           | 785          | CTTTTCAAGCGCAACCAAGGGGATGAGCCTGTTCACCAATGCTCCATCAACAGCGCGGACCA    | 844            |        |             |
|              |              |   |                |        |             |
| Db           | 1187         | ccctcaaggtccagccaggaagctgtgaagctgtctcccaactgcccccttcaaaagcgcgtccc | 1246           |        |             |
| QY           | 845          | CTTTCGAAGGGGCGACCAACTGTGTGTGGCGCAATGGCTACTACAGAGCAGACTGGACC       | 904            |        |             |
|              |              |   |                |        |             |
| Db           | 1247         | cttcaagagcgtctcccatctgcaactgtccgagctgtgctattacacgaagactttgact     | 1306           |        |             |
| QY           | 905          | CCCTGACATGCCCTTGGACACCAATCCCTCGCGGCCCAAGGCTGTGATTTCCAGTGTCA       | 964            |        |             |
|              |              |   |                |        |             |
| Db           | 1307         | ccccgaaggtgtgtgtgcatagtgtctccatcagaagccctcgaaatgtcatctcatatgtga   | 1366           |        |             |
| QY           | 965          | ATGAGACCTTCCCTGTCGCGAGTGGACCCCTCCCGCGACTCCGAGGCGCGAGAGACCA        | 1024           |        |             |
|              |              |   |                |        |             |
| Db           | 1367         | atgagagcatctactctctagatgtgcccacttccaaagagaagaccggtgtggcgagatgatg  | 1426           |        |             |

[illegible][illegible]

|    | Key   | Location/Qualifiers |
|----|---|---------------------|
| FF | CDS   | 1..2973             |
| FT |   | /*tag= a            |
| XX |   |                     |
| XX |   |                     |
| PN | DE4233782-A.  |                     |
| XX |   |                     |
| PD | 14-APR-1994.  |                     |
| XX |   |                     |
| PF | 07-OCT-1992;  | 92DE-4233782.       |
| XX |   |                     |
| PR | 07-OCT-1992;  | 92DE-4233782.       |
| XX |   |                     |
| PA | (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.                             |                     |
| XX |   |                     |
| PI | Holtlich U, Ruebsamen-Waigmann H, Strebhardt K;                     |                     |
| DR | WPI: 1994-127194/16.  |                     |
| XX | P-PSDB: AAR51899.   |                     |
| XX |   |                     |
| PT | Human embryonal Kinase 2-receptor protein - useful in tumour        |                     |
| PT | diagnosis and therapy   |                     |
| XX |   |                     |
| PS | Claim 4; Page 7-10; 11pp; German.                                   |                     |
| XX |   |                     |
| CC | RNA from human embryonic tissue was isolated. With the use of       |                     |
| CC | primer P6(4) PTR-specific cDNA was synthesised. The cDNA was        |                     |
| CC | amplified using primers P6(4) and N5. A 2097 bp DNA fragment was    |                     |
| CC | obtained. Primers E3, P12 and E6 were then used in the isolation of |                     |
| CC | the C-terminal of the HEK2 receptor gene.                           |                     |
| XX |   |                     |
| SO | Sequence 3751 BP; 739 A; 1150 C; 1123 G; 739 T; 0 other;            |                     |

|    |  |              |               |            |              |                    |
|----|--|--------------|---------------|------------|--------------|--------------------|
|    | Query Match  | 53.5%        | Score 1583.4; | DB 15;     | Length 3751; |                    |
|    | Best Local Similarity  | 72.6%;       | Pred. No. 0;  | Mismatches | 766;         | Indels 33; Gaps 4; |
|    | Matches 2116;  | Conservative | 0;            |            |              |                    |
| Oy | 10 GCCGGGAAGAAGAACTTATGATGCATCCACTACAGGAGCTCGAGTCGTGGCGTGAGATGGTG 69     |              |               |            |              |                    |
| Db | 85 ggcgtcggaagaaacctctcatgaccacaatggtaacatcctgaglttgcygcaactc 144        |              |               |            |              |                    |
| Oy | 70 CATCTCCATCATCAGGGTGGGAGAGGGTGAATGCTACGATGAGAACATAACACGATCCGC 129      |              |               |            |              |                    |
| Db | 145 catccaagaagtgggttgggaaggtagtgctagtcgatgagccatgatccatccgcg 204        |              |               |            |              |                    |
| Oy | 130 ACGTTCCAGAGTGTGCAAGCTGTTTAATGTCAGCCAGAACACTGCCTACGACCAATT 189        |              |               |            |              |                    |
| Db | 205 acataccaggttgttaattgtgcgcgaitaagccagaaacaactggtcttcgcacgggttc 264    |              |               |            |              |                    |
| Oy | 190 ATCCGGGCCGCGGGGGCCCAACCGCATCCACGTCGAGATGAATTAATTTCGTGGCTGATCC 249    |              |               |            |              |                    |
| Db | 265 atctggcggcggaatgtgcagcgggtctaagcyggagcttaagttactgtgcgtactgc 324      |              |               |            |              |                    |
| Oy | 250 AGCACATCCCCAGGCGTGCCTTCCTCCGCAAGAGAGACTTAACTCATATCATATGAG 309        |              |               |            |              |                    |
| Db | 325 aacagcatcccacaatatccccgcgtccctgcgaaggagaccttaacctcttctaactagag 384   |              |               |            |              |                    |
| Oy | 310 GCTGACTTTGACTCGGCGCACCAAGACTTCCCACATGSATGGAATTCATGCAGGTGAAG 369      |              |               |            |              |                    |
| Db | 385 gtgcagcagcgaatgtgcgtccacgctctccctctctgatatggaaacccctacgtgaaa 444     |              |               |            |              |                    |
| Oy | 370 GTGGATACCATTGGACCGCGACGAGACTTCTCCAGGTGGACCTGGGTGGCCGCTCATG 429       |              |               |            |              |                    |
| Db | 445 gtgcagcacatgtgaccccgatlgagsgcttctgcgcctlgatgctgcgcg----- 494         |              |               |            |              |                    |
| Oy | 430 AAAATCAACACCGAGAGTGCAGAGCTTTCGGACTGTGTCCCGACGGGCTTACTGTGGC 489       |              |               |            |              |                    |
| Db | 495 --tgtcacaccaagaagtgtgcagacttltggcaccattccaagaagctgtgtcttaactggcc 552 |              |               |            |              |                    |
| Oy | 490 TTCCGAGCATATGGGGGCGATGTCCTCATCGCGCGGCGTGTTCATCCGCAAGAGC 549          |              |               |            |              |                    |
| Db | 553 ttccagagccagggcgcctgtgcattgtcgtcatacttcgcgtgcgcgtctctcaagaagtgt 612  |              |               |            |              |                    |

|    |      |   |      |
|----|------|---|------|
| QY | 550  | CCCCCATCATTCGAATATGGCGCATTTTCCAGAAACCTGTGCGGGGCTAGAGACACA                 | 609  |
| Db | 613  | gcatccaccaccggaagcgttcgcactctcccgagacactcaactcgtgggagagccacc              | 672  |
| QY | 610  | TGCGTGGTGGCGCCGGGGGAGCTGGATGGCAATGGCGGAAGAGGTGATGTACCCATC                 | 669  |
| Db | 673  | tgcgcggtccattgtcctcgtgcaactgtcaactcaagccgctggaggtgtcgtgtccactc            | 732  |
| QY | 670  | AAGCTACTGTAACTGGGGAGCGCGAGTGGCTGGTGCCATCGCGGCTGCATGTGCAAA                 | 729  |
| Db | 733  | aagctcactatgcaagcgcgtatggggagtgtgagtgtcgtgtgggtgcgtcgaacctgtgc            | 792  |
| QY | 730  | CGAGGCTTCGAGGCGTGTGGAAGATGGCACCCTGTCCCGAGGTGTCTCATCTGGACTTTC              | 789  |
| Db | 793  | accggtccatgtgaccagctgtccaaagagttcccaatgtgcgccctgttccctctggagctac          | 852  |
| QY | 790  | AAGGCAACCCAGAGGAGATGGAGGCTGTACCCACTGTGCCATCAACAGCGCGACCACTCT              | 849  |
| Db | 853  | aaggtgaagcagggagaggggcccgtcctcccatgtccccccaacgcgtatacactcc                | 912  |
| QY | 850  | GAAGGGGCGACCAATGTGTGTTCGCGCATAGGATAGCATAGAGACAGACACTGGACCCCTG             | 909  |
| Db | 913  | ccagcgcgcagcagctctgtgactgtgcaataaattctacocgtgtgcagctcgcgactctcg           | 972  |
| QY | 910  | GACATGCGCTGCACACACCATCCCTCGCGGCCCCAGGCTGTGATTTCCAGTCTCAATGAG              | 969  |
| Db | 973  | gacagttgctgttaccacocgtgtccacttccaccacccgaggtgtgtacttccaattgtgaatga        | 1032 |
| QY | 970  | ACCTTCCCTCATGCTGATGATGGAGACCCCTCCCGCGACTCCGGAGCGCGAGAGAGACCTCGTC          | 1022 |
| Db | 1033 | acctcaactgtatcctctgtgagttgagctccgcggagacttgggtgttccggagatgaactctcg        | 1092 |
| QY | 1030 | TACACATCATCTCTGAAGAGTGTGGGTGGCGCGCGGG-----TGCGTGCACCCGCTGC                | 1083 |
| Db | 1093 | tacaaattgtcatctgtgcaagaaagtgtgcataatgtgggtcgtggaggggtccagctcgcctcaagcgtgt | 1155 |
| QY | 1084 | GGGGCAATGTACATATGACGACACACGCGCAGCTAGGCTGTACGAGGACGACCATTTATATC            | 1143 |
| Db | 1153 | gatgacaacgctggaggtttgtgtcctcgtcagactgtgacctgtcgagagcccggtgtccacac         | 1212 |
| QY | 1144 | AGTACCTGTGGGGCCACACCCAGTACACTTGTGAATCCAGGCTGTGAAGGGGTACT                  | 1209 |
| Db | 1213 | agccaactgcgtgggcaccaacgcgtatacaacttggagtgcaagcgggtatcaaggtgtctcg          | 1271 |
| QY | 1204 | GACGAGAGCCCTCTTGTGGCTGTCAAGTTGCGCTGTGTAAATCATCCACCAACCAAGGCACT            | 1263 |
| Db | 1273 | ggcaagagcctctctgcgcctcgtgtatgtgcgctgtgaatatcaaccacaacagagctgccc           | 1332 |
| QY | 1264 | CCATCGGCGAGTGTCTATCATGTGCATCAGGTGAGCGGACCGGATGAGCATTTACCTGTGCG            | 1332 |
| Db | 1333 | ccgtctgtagatgtcccaactaagcgtctgtcaagagactcagagcagcctcactcaactctcc          | 1392 |
| QY | 1324 | TGTGTCCAGCCGGAGTACAGGCCAATGGCGGTGTACTGTGACATATGAGCGTGCAGTACATATG          | 1389 |
| Db | 1393 | tgggaccccccaagatgggcaccaagggatcatctgtgactaataagatgtgaagtactgtag           | 1455 |
| QY | 1384 | AAGGAGCTCATGTGATATCAACAGCGCACGACCATTAATAAAGCGCCACCAACACGGTGTCACGGGC       | 1443 |
| Db | 1453 | aagagcgaagggcatctgcgtctccacagatgtaccagcagatgaactccgtgtgagctgtgacggg       | 1512 |
| QY | 1444 | CTCAAAAGCGCGGCTATCATGTCTTCCAGAGTGGCGGGACGCACTGTGGCAGGCTTACGGG             | 1503 |
| Db | 1513 | cttcggtctgacgcgcgtgtgtgtcctcaggtgtcgtgtccgcagtaagctgtgatactggg            | 1571 |
| QY | 1504 | CGCTACACGGCAAGATGTACTTCCAGACCATATACAGAAAGCCGAGTACCAAGCAAGCA--             | 1561 |
| Db | 1573 | cagtaacagccgcctctgcgcagattgtgaagccacaagtgtgaagaggtctgtgggcccagag          | 1632 |
| QY | 1562 | -TCCAGGAGAGTTGGCACTCATCATCATGAGGCTCTCGCGCGCTGGCTGTCTCTCATTT               | 1620 |
| Db | 1633 | cttccagagagcaggtctccctccatctgtgtgggtcctgcgtcaacagcttggggttctctgtgtgt      | 1692 |
| QY | 1621 | GCTGTGGTGTGCATAGCCATCTGTGTGTAAACAGACGGGGGTTTGAAGCTGTGCATCGGAG             | 1680 |







Db 2255 ttcgggtctcccgctcttttggaggatgatccagccgagcccccataccagctccctg 2314  
 QY 2305 GCGGGAAGTTCCATCCGCTGACAGACCCCGAGACCATCATAGTACGGGAATTGACC 2364  
 Db 2315 ggaaggacagatcccatcaggtcagtcagctctcagagccatccgcaataatcag 2374  
 QY 2365 TCGCGAGTGAATGTTGAGTACGAGCTTTGTCACTGTGGAGGTGATGCTTATGGGAG 2424  
 Db 2375 tcggccagcgcgtggtgagatcagcatcgtcatctggtgagatgagctcctacggagg 2434  
 QY 2425 GCGCCCTACTGGAGATGACCAACAGGATGTATCAATGACATTTGAGGAGATACCG 2484  
 Db 2435 cgacctctctggaacatctccacacagatgtagtcaacgcgtgagagacagatccag 2494  
 QY 2485 CTGCGACCGCCCATGAGTACGCGCCGACCGCTGACCACTCATGATGATGAGTGGAG 2544  
 Db 2495 ctgcacaccccccagactgcccacacagcatctgacacagctgtagctgagctctgg 2554  
 QY 2545 AAGGACCGCAACACCGCCCAAGTTGCGCCAAATTTGTCAACACGGTACGACAGATGATC 2604  
 Db 2555 cgggacgcgcaacctgcgcccaagttctgcacagatctgtaacacagcctgagcaagctgac 2614  
 QY 2605 CGCAATCCCAACAGCTCTCAAGCCATGCGCGCCCTCTCTCTGTGACATCAACCTGCCGTG 2664  
 Db 2615 cgcacatctgcccagcctgaaagttcatcgccagcgtccagtgctcccccagccgctc 2674  
 QY 2665 CTGACCGCAGATCCCGGCTACACAGCTTTAACACGCTGACAGTGGCTGAGAGCC 2724  
 Db 2675 ctgagccgcgcgtctgcagatctacacacctctacacacgttggaagctgtagatg 2734  
 QY 2725 ATCAAGATGGGGAGTACAGAGAGAGCTTCCGCAATGCCGCTTCACTCTTTGACGTC 2784  
 Db 2735 atcaaatctggaagctgacaaaggaagaaactctgtaaacgcgtctgcctcttgaac 2794  
 QY 2785 GTGTCTCAGATGATGATGAGAGGACATTTCTCCGGTTGGGTTGCTTGGCTGGCCAG 2844  
 Db 2795 gtgcccacagatgacagacagagacccgctcaagatagagtgtagcagcagcagcag 2854  
 QY 2845 AAAAAAATCTTGAACATTCAGTTCAGTGTGATGCGGCGCAGATGACAGATTCAGTCTGTG 2904  
 Db 2855 aagaagatctctgagcagcatctcagatgagatgagctgcagatgaaacacagcctgcggt 2914  
 QY 2905 GAGGTTTGAC 2914  
 Db 2915 cbggtttgac 2924  
 RESULT 12  
 AA090658  
 ID AA090658 standard; cDNA; 3591 BP.  
 AC AA090658;  
 XX  
 DT 11-NOV-1995 (first entry)  
 XX  
 DE Eph-related PTK Cdk10+ cDNA.  
 XX  
 KW Cdk10+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
 XX  
 OS Gallus sp.  
 XX  
 FH Key  
 FT 2, 2968  
 FT CDS /-tag- a  
 XX  
 PN W09515375-A.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 07-SEP-1994; 94MO-US10140.  
 XX  
 PR 03-DEC-1993; 93US-0162809.

XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Pasquale EB, Sajjad FG;  
 XX  
 DR MPI: 1995-215256/28.  
 DR P-PSDB: MAR75710.  
 XX  
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 XX cancer.  
 XX  
 PS Claim 2; Page 78-82; 129pp; English.  
 CC  
 CC Novel Eph-related PTK cDNA clone Cdk10 (given in AA090656) and a  
 CC variant clone, Cdk10+ (AA090658), whose product contains a 15-amino  
 CC acid insertion in the juxtamembrane domain, were isolated from a  
 CC chick embryo library in lambda 911. Cdk10 and Cdk10+ may  
 CC originate from the same gene by alternative splicing. Cdk10  
 CC expression was prominent in the kidney, and to a lesser extent in  
 CC the lung.  
 SO Sequence 3591 BP; 753 A; 1112 C; 1042 G; 684 T; 0 other;  
 Query Match 52.1%; Score 1543.4; DB 16; Length 3591;  
 Best Local Similarity 72.3%; Pred. No. 0;  
 Matches 2114; Conservative 0; Mismatches 746; Indels 63; Gaps 6;  
 QY 43 GCGACTGCTGCTGGCTGGCTGATGCTGATCCTTCATCAAGGCTGGGAGAGGACTGGC 102  
 Db 59 gtgacctcggagctgcatgtagacacccatccgagagcgggtggaagaggtcagtggt 118  
 QY 103 TACGATGGAACATGAAACAGATCCGACGTTACAGCTGTGTTAGTCAAC 162  
 Db 119 taagcagagctatgacacccacccgacatcacaggtgtgcaacgtcggagagccaac 178  
 QY 163 CAGAACACTGTGCTACGAGCAAGTTATCCGCGCGGCGGCGGCGGCGGCTTCACCTG 222  
 Db 179 cagaacacactgcttcgcaacaaagttcatctcagcagagctccaggtgctcagtg 238  
 QY 223 GAGATGAGTTTTCGGTGGCTGACTGCACAGCATCCCGAGCGTCCGCTCTGCAAG 282  
 Db 239 gacgtgaaatctacgtgtaggactgcaacagatcccaacatccctggtctccgcaa 298  
 QY 283 GAGACCTTCAACCTTATATGATGAGGCTGACTTGAATGGCCACCAAGACCTTCCC 342  
 Db 299 gagacctcaacctctctatataatgtagtcaagatctgctctgccaatagccct 358  
 QY 343 AACTGATGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 402  
 Db 359 tcttgatgtagaaccctatactcaagtgatatacaatctgctcggatgagatcttccc 418  
 QY 403 CAGGTGACCTGGTGGCGCGCTCATGAATAATCAACACCGAGTGGAGCTTGGACT 462  
 Db 419 aaactgagatctccgcg-----tgtaacacacaggtgcgacgtcttggcgcg 466  
 QY 463 GTGTCCCGACGCGCTTACCTGAGCTTCCAGGACATGAGCTGCGCTGATGCTCTGCT 522  
 Db 467 ctctcagaagatgcttctatctgcttccagagcccggtggcgtgcagatctccatc 526  
 QY 523 GCGGTGCGTCTTCTTACCGCAAGTGGCCCGCATCATCAAGAAATGGCCCATTTCCAG 582  
 Db 527 tccgtccgggtctctctaaagaatgctcacaacacacatctggtcttgatctcccg 586  
 QY 583 GAAACCTGTGCGGGGCTGAGAGACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642  
 Db 587 gagaacctcaacgggggtgtagccacgtctggtctatctgctgcgggacacgtcacc 646  
 QY 643 AATGGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 702  
 Db 647 aacgcagtggaagtgctctgcccctgaaagctgtaacagcaggtgtagcgtgtagtg 706  
 QY 703 GTGCCATCGGGCGCTGCATGTCGAAGACGAGCTTGAGAGCGCTTGAGAAATGACCGTC 762



|    |      |  |      |
|----|------|--|------|
| Db | 707  | gtgcctctgggaagcgtgcacgtctgtcctcgtggtacgaagccatgaagatacccaag          | 766  |
| Oy | 763  | ttgcggaggtttgcattttgcgaccttttcaagaccacacacagggatgagcctttaccac        | 822  |
| Db | 767  | tgcacaagaatgcgcgcggggagcgtttcaataatccaagaaggcgagggccctctccccc        | 826  |
| Oy | 823  | ttgtccatcacaacagcccgaccactttcttgaaaggcccaacactgtgtcttgcgcgaatggc     | 882  |
| Db | 827  | tgccctcccaacaacgcgcaccaacgcgcggggcagcagctcaagctctgcataatctcgaagcgc   | 886  |
| Oy | 883  | tacttccagagaagaagcggaccaccccttgagacactgtgcctcgcacaaacatcccctccggccc  | 942  |
| Db | 887  | ttcttcgcgaagaagaagcggaccaccccgacagaagcgctgcgaacacagtgtgcctcaagcccca  | 946  |
| Oy | 943  | cagcgtgtgatttttcacgttcattatgacactccctcatgcttgagtgtagacccctcccccgc    | 1002 |
| Db | 947  | cgcagcgtcatctctccaacgttgatbagaagcgtcgtctgtgtctcgtatgtgaatgagcgcag    | 1006 |
| Oy | 1003 | gactccggagagccgacagagaccatctgccttcacaaacattcatctcagaagctgtggcgtccggc | 1062 |
| Db | 1007 | gacgcggggcgggcgaggatgaaacctgtctctccacaagctcatctcgaagaagtgaagctggag   | 1066 |
| Oy | 1063 | cgggggctcgtgcaccgcgctgcgggggacaattgtacagtagcaccacgcacgt-----         | 1115 |
| Db | 1067 | cggcgcgctgtgcagcgcgtgcgaagcaacgttgaagttctgtgcgcgcgaactgggcctc        | 1126 |
| Oy | 1116 | --agccttaccgagcaccgcatcttgcatttgcattgacactgcgtggccacacccagatcac      | 1173 |
| Db | 1122 | actgtgcctcactgaagagcagcatctacatcagcaagatgtagtggccaccgccagtaacac      | 1186 |
| Oy | 1174 | tttcgacatccagcctttgaaacggcgtttactgacacagacccttctgccttcagtccccc       | 1233 |
| Db | 1187 | ttcgaagatccagcgctgagatgtcatctccaagaagaagcccttaccctcccatcttgc         | 1246 |
| Oy | 1234 | ttctgtgaacatcaccacacacacagagctccatgcggcagtgcttcacatcagatagctg        | 1293 |
| Db | 1247 | ttcgttaaacatctcgaacacacagcagcccatctgcgcgtgcgcacatatgcatctgac         | 1306 |
| Oy | 1294 | agccgcaccccttgaaacagatttaccctgtcgtgtccacccgacaccccaatggcgtg          | 1353 |
| Db | 1307 | agcagccacgggaagcagatgacatctgatactgatactcccccgaagaagcctcaagctgcatc    | 1366 |
| Oy | 1354 | atccttgacattgacctgcagcttactgtatgaaag---gagttcagctgagatcaaacggccaca   | 1410 |
| Db | 1367 | attctgcactatgaatacctaagtaactccgaagaagcgaaggtcgaagctatgcgaac          | 1426 |
| Oy | 1411 | gccattaaaaagcccccacacacacgcgtacg-----ggcctcaaacccggccatttat          | 1464 |
| Db | 1427 | actgtcaacacagcagaagaactcgtgtgcgtcgtgagcagactgaaagccaatgtctgtaac      | 1485 |
| Oy | 1465 | gtctttccagagtgccgggacgcacactgtgtggcagcctacagggcgcttaccacggcgaagtac   | 1524 |
| Db | 1487 | atgtgtcagcgcgcgcgcgcgaagctgtgtctgtatgaatcagcgcgtacacgcctcccccag      | 1546 |
| Oy | 1535 | tttcagacacatgacagaaagccgacttaccagacagacagcttccagggagttcccatctatc     | 1584 |
| Db | 1547 | ttccgaagacatgcggaagatgtgtctccacacgaagacattccagggagcttctctcatc        | 1606 |
| Oy | 1585 | atgcgcttccctgcggcgcgtggcctgttcttctctcatgtgtgtgtgtatcgtccatcgtg       | 1644 |
| Db | 1607 | gtgtgttcagccacgcgcgcgcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt       | 1666 |
| Oy | 1645 | tgcttaacagacgggggtt-----tgagcgtctgcagctgcgtgcgtgacacagacacgtctca     | 1698 |
| Db | 1667 | tgcttcaagaagaaggatgtgtacttgatacaactcctctcgttctcctttgggagaagcag       | 1726 |
| Oy | 1699 | gacttaccacagtgccgcaca-----taaccacagcagtg                             | 1731 |
| Db | 1727 | cgaacacgacagatcccgagatgaacagagaagctgtcagcaataatgtcatctccttggatg      | 1786 |
| Oy | 1732 | aagattctacatcgattctttactctacagacagaccccaacgagggcagctggagattggcc      | 1791 |

|    |      |  |      |
|----|------|--|------|
| Db | 1787 | aaggtcacattgacccttcaactatgaaagcccaatgaagctgtccggaaattcgcc          | 1846 |
| Qy | 1792 | AAGGAATTGACATCTCTGTTGTCAAAATTGAGCAGGTGATCGAGCAGGAGATTGGC           | 1851 |
| Db | 1847 | aagaagattgatatactcttcgtgtgccaattgagagagtgaaatgtagcagagagattggt     | 1906 |
| Qy | 1852 | GAGGTCTGCAGTGGCCACTGAAAGCTGCCAGGCCAAGAGAGGAGATTTTGTGGCCATCAAG      | 1911 |
| Db | 1907 | gaagtgcccggtgagcgtctgaagcgtgctggccgcgcgtgagatcttctgtgcatcaag       | 1966 |
| Qy | 1912 | ACGGTCGAAGTGGGGCTCTACAGCGAAGACGCGCGGGACTTCTGAGCGAAGCCTCATC         | 1971 |
| Db | 1967 | acaacgaaggtgggtctacacagagagagcagcgcgagacttccctgagtgaagccagatc      | 2026 |
| Qy | 1972 | ATGGGCCAGTTTGACCAATCCCAACGTCATCCACTTGGAGGGGTGTGTGACCAAGGCA         | 2031 |
| Db | 2021 | atgggcacagtttcgacaccccaatcatlccactcggagagggcgtgtgtgaccaagagccgc    | 2086 |
| Qy | 2032 | CCTGTGATGATCATCAACGAAATTGATGANAAGGCTCCCTGGACTCTTTCTCCGGCA          | 2091 |
| Db | 2087 | ccctgacagatcacacacagagtttcatgagaactgctgctctgcactcttccctcgctg       | 2146 |
| Qy | 2092 | AAOCATGGGCGAGTTCACAGTCATCCACCTGTGGGCAATGTTGGGGCAATCCAGCTGAC        | 2151 |
| Db | 2147 | aatgattgagcagtttcaagctatccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt       | 2206 |
| Qy | 2152 | ATGAGTACCTGGGCGAGCATGAACTATGTTTACCGCTGACCTGGCTGCGCCGCAATCTC        | 2211 |
| Db | 2207 | atgaagatcccttcagagatgaatgaactacgttgacacggagactgtgcgcgcaacatctg     | 2266 |
| Qy | 2212 | GTCCACAGCAGACCTGCTGTCAGAGTGTGCGGACTTTGGGCTCTCACGCTTTTCAGAGAC       | 2271 |
| Db | 2267 | gtcaacagagaactgtgtctgcaaaagtgtctgaattcgggctcccgcttlttgagaggt       | 2326 |
| Qy | 2272 | GATACCTCGAGACCCACCATCACACAGTGTCCCTGGCGGAAAGTTTCCCATCGCTGGACA       | 2331 |
| Db | 2327 | gattccagccgagcccccctacacacagctcccttgggaggaagatccccaatcaggtgagaa    | 2386 |
| Qy | 2332 | GGCCCGGAAGCCATCCAGTACCGGAATTCACCTCCGCGAGTGTGATGTGTGGACTCTGCGC      | 2391 |
| Db | 2387 | gtcttcgtaggcctctgctccacacgcaaatlccagctgcgcagcgcgtgtgtgagctacgc     | 2446 |
| Qy | 2392 | ATTGTGATGTGGGAGTGTGATGTCTCATGTGGGAGCGCGCCCTACTGGGACATGACCAACAG     | 2451 |
| Db | 2447 | atcgtcaatgtgggaagtgtgattgtcttcaacgggggcgaacctactgtggacatgtccaaacag | 2506 |
| Qy | 2452 | GATGTATTAATGCCATTTGAGCAGACACTATCGGCTGCCACCGCCCATGAGACTGCCGACG      | 2511 |
| Db | 2507 | gattgtgatcaacggtgtgagcagaggtlccgcgtccgcaccccccaatgagactgtccca      | 2566 |
| Qy | 2512 | GCCCTGACCAACTCATGTGCGACTTTTGGAGAGACCGCACCAACCAACCGGCCCAAGTTC       | 2571 |
| Db | 2567 | gcaatgcacagactgtgagctgtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt      | 2626 |
| Qy | 2572 | GGCCAAATTTGTCAACACGCTAGACAGATGATCCGATCCCAACAGCCTTCAAGGCATG         | 2631 |
| Db | 2627 | gcaacagattgcaacaacgctgtgcacaagctgatacgcgaatgtgcagacgtgaaggtatcc    | 2686 |
| Qy | 2632 | GGGCGCCTCTCTGTGGCATACACCTGCGGTGCTGACCGACGACGACCATCCCGACTACAC       | 2691 |
| Db | 2687 | gcccagctgtccaagtcgtgtcttcccaacgcgctctcctgtgacgcacacgtgtccgattacac  | 2746 |
| Qy | 2692 | AGCTTTAACACAGGTGAGCAGAGTGGCTGAGGAGCCATCAGATGGGGCAGTACAAAGAGAGC     | 2751 |
| Db | 2747 | accttaccacacgtgtgagagactgtgtgattgcatcaaaatgtgtgcgcgtglaaagagaac    | 2806 |
| Qy | 2752 | TTCCGCAATGCCGCTTACACTCTCTTGTGAGTGTGCTGCACATGATGATGTGAGAGACATT      | 2811 |
| Db | 2807 | ttcgtccaacgcgcgtcttcgctctcttgcacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt     | 2866 |
| Qy | 2812 | CTCCGGGTTGGGGGTACTTTTGGCTGGCCACAGAAAAAATCTGACACGATATCCAGGTG        | 2871 |
| Db | 2867 | ctaaggaataggaatgacgtatagcagggccacagaagaagatctcttcagcagcatcagagac   | 2926 |



|    |      |  |      |
|----|------|--|------|
| Db | 1696 | ttgactatcagatgtaagtaactctttgagaagtaaaagcatccctccacgttcaacagc       | 1755 |
| QY | 1417 | AAAAGCCCCACAAACAGGCTACAGGGGCGTCAAAAGCGGCGCCATCATGTTCACAGTG         | 1476 |
| Db | 1756 | cagaagaatctgttaacaactgagacgtgacgtccagcccgacccgttatgtatgctcaggtc    | 1815 |
| QY | 1477 | CGGGACGCGCACTGTGGCAGAGCTACGGGGCCCTACAGCGGCAAGATGTTACTTCCAAACATG    | 1536 |
| Db | 1816 | cgaggtccgcacagtaagtaagttatcagcacagtaaacgcgccacgtgtgaattgagaacag    | 1875 |
| QY | 1537 | ACAAAGACCCGAGTACCGAGAC---AAGCATCCAGAGGAAGTTGCCACTCATATGAGGCTCC     | 1593 |
| Db | 1876 | agttaaaagaggtctcgaagggtcccaagcaagcttcaagaagcaagcttccctaatgttggatcc | 1935 |
| QY | 1584 | TCGGCCCGCTGGCGCTGGTCTTTCATCTGCTGTGGTTGTTCATCGCCATCTGTGTAAACAGA     | 1653 |
| Db | 1936 | acgttaactgtgcttgccttcaacatggtgcgtcgtcgtgtatgtatgtccttgcctcaag      | 1995 |
| QY | 1654 | CGGGGGTTTGGAGCTGGCTGTGACTCGGTGACTACAGGAAACATCCATCAACACAGTGGC       | 1713 |
| Db | 1996 | aagcagcgcccaagggccctgtatgagaataacaaggaagtgttcagcaat-----           | 2044 |
| QY | 1714 | CACATTAACCCCAAGGATGAAGATCTACATCGATCTTTCACCTACGAGGACCCACAGAG        | 1773 |
| Db | 2045 | -acgtgcgcccaagagtgaaagttacatgttaagcccttaccctacagagatcccaatgag      | 2103 |
| QY | 1774 | GCAGGCGGGAGTTTGGCAAGGAATTTGACATCTCTCTGTGTGAAAATTTGACAGAGTGATC      | 1833 |
| Db | 2104 | gccgcgccgaaggttcgcaccaagagatcagatgtgtccgtgcgtcaagatccgaagaaagtgtt  | 2163 |
| QY | 1834 | GGAGCAGGGGAGTTTGGCGAGAGTCTGCAGTGGCCACCTGAAGCTCCAGGCAAGAGAG         | 1893 |
| Db | 2164 | ggagctcgggagagtttgggagagtgctgcgggtctgaaactgcgcgcgcgcggagag         | 2223 |
| QY | 1884 | ATCTTTGTGGCCATCAAGACGCTCAAGTGGGCTACACGGGAACACAGCGCGGGACTTC         | 1953 |
| Db | 2224 | gtgttcgttgagcatalcaagaacactgaagagtgtgtatcaacggaagacagccggcggaactc  | 2283 |
| QY | 1954 | CTGAGCGAAGGCTCTCATCATGAGGGCCAGTTTCGACATCCCAAGTGTATCCACTTGAGAGGT    | 2013 |
| Db | 2284 | ctgagttgagagcttccatcatalggttcaatttgacacatccaaatataatccgttctagaggc  | 2343 |
| QY | 2014 | GTCTGATCAAGACACACCTGTGATGATCATCACCGAGTTATGGAAGATGCTCCCTG           | 2073 |
| Db | 2344 | gtgtgcacaaagaatcgtccacgtacgtatccactgaagttatgtgaagaactgtgtgcctgt    | 2403 |
| QY | 2074 | GACTCTTTTTCGGGGAAAAAGATGGGCGAGTTACACGTATCATCCACTGGTGGCAATGCTT      | 2133 |
| Db | 2404 | gactcttcttccataaggtccaaatgaagggcaattcaacagttcaacagcttgcgttgagatgtg | 2463 |
| QY | 2134 | CGGGGCATCGCAGCTGGCATGAAGTACTGTGGCAGACATGAATGTTCAACGTTGACCTG        | 2193 |
| Db | 2464 | cgttgcattgtgtgcgcagatgaagtacttgtctgagatgaactacgttgaaccgttgaactc    | 2523 |
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| Db | 2524 | gctgcgccgaacatctctgttcaacagtaactgtgtctgcaaaagtatctgaacttgggtctc    | 2583 |
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| Db | 2584 | tccgcgttccctggagagagacccctcagaccaccacttaacacagcttccctggtgtggagag   | 2643 |
| QY | 2314 | TTTCCCATCGCTGTGAGACGCCCGGGAACCCATCCAGTACCGGAAGTTCACTCGGCCAGT       | 2373 |
| Db | 2644 | atccctatcgttgtgacgcgcccaagggccatagactatcggaaattcaagctgtctcagc      | 2703 |
| QY | 2374 | GATGTGTGAGACTTCAGCATTTGTCATGTGGAGAGTAGTATCCATGGGGAAGCGCCCTAC       | 2433 |
| Db | 2704 | gatgtctggaaactcaaggaatcgtcaatgttggagaggtcaatgaactcaaggaagagacataac | 2763 |
| QY | 2434 | TGGGCATGAGACCAACGAGATGTTAATCAATGCCATTGAGCAGAGACTATTCGGCTGCCACG     | 2493 |

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|------------------|---|---|-------|
| Dd               | 2764  | tggagacatgagcaaacccgatgtgcattcatcaatgcccgtagagcaagaactatcgtttaccaccc  | 28233 |
| Oy               | 2494  | CCCATGAGCTGCCCGAGCACCCTTCGCACCAACTATCTTGACTGTGGGACAAGAAGCACGC         | 25533 |
| Dd               | 2824  | cccccttgaccttcccgaacgagcttcgtcacccagtcatctctggaactgttgtggtggaaccgg    | 28833 |
| Oy               | 2554  | AACCAACGGGCCCAAGTTCCGGCCAAATTGTCTAACACGCTGTAGACAGATGATCGGCNAATCCC     | 26133 |
| Dd               | 2884  | aacctcaggccccaagttctctcccaaatcglctaacaacgcttagaagaattatccgcaatgct     | 29433 |
| Oy               | 2614  | AACAGCCTCAAAAGCCATGAGCGCCCTTCTCTCTGGCATFAAECTGCGCTGCTGGACCGC          | 26733 |
| Dd               | 2944  | gccagccctcaaggtcatcgcacgtgcagtgcccccatctggaatgtcccaagccccctcttagaccgc | 30033 |
| Oy               | 2674  | ACGATCCCCGAGCTACACAGCTTTTAACACAGGTGACGAGAGTGGCTGGAGGCATCAAGATG        | 27333 |
| Dd               | 3004  | acggctccagaatttaacgaacctccaagaagtgtyggagcattgctatgacatagcataagatg     | 30633 |
| Oy               | 2734  | GGGCAGTACAAAGAGACGTTTGGCCAATGCGCGCTTCACTCTTTGACGTGCTGTCTAG            | 27933 |
| Dd               | 3064  | gggaagatctaaagaagagctctcgttcgtgtgcggtttcttgctccttgaacctgtgtgcccag     | 31233 |
| Oy               | 2794  | ATGATGATGAGGAGGACATTTCCTCGGGGTTGGGGGTGACCTTGGCTGGCCACAGAAAAAATTC      | 28533 |
| Dd               | 3124  | atgactcgaagaagatctcgtaagaatcgggtggtacatttggccgaccaagaagaagatc         | 31833 |
| Oy               | 2854  | CTGAACAGTATTCAGGTGATGCGGGCGCAGATGAACACAGATTTCAGTCTGTGGAGGTTTGA        | 29133 |
| Dd               | 3184  | ctcagcagtatccagagacatgctgcgctgcagatgaaccagaactgcccgtgcaggtctga        | 32433 |
| Oy               | 2914  | CATTACCTGCTCGCTCGCTACACTTCTTCTCTCAAGCC                                | 2949  |
| Dd               | 3244  | cgtcagctccagcaggtgaggtgtggtcccccgggac                                 | 3279  |
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| ID               | AAQ90982  | standard; cDNA to mRNA; 4027 bp.                                      |       |
| XX               | AAQ90982;   |   |       |
| AC               | 24-NOV-1995   | (first entry)   |       |
| XX               |   |   |       |
| Dt               |   |   |       |
| XX               |   |   |       |
| Kw               | Protein p140; insulin; tyrosine phosphorylation; ss.                |   |       |
| XX               |   |   |       |
| OS               | Rattus rattus.  |   |       |
| XX               |   |   |       |
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| FT               | CDS   | 262..3243   |       |
| XX               |   | /*tag= a  |       |
| PN               | EP659883-A.   |   |       |
| XX               |   |   |       |
| PD               | 28-JUN-1995.  |   |       |
| XX               |   |   |       |
| Pf               | 24-NOV-1994;  | 94EP-0118524.   |       |
| XX               |   |   |       |
| PR               | 24-NOV-1993;  | 93JP-0315806.   |       |
| XX               |   |   |       |
| PA               | (ONOY ) ONO PHARM CO LTD.   |   |       |
| PI               | Kitagawa K, Ohno H, Tajima H;                                       |   |       |
| XX               |   |   |       |
| DR               | WPI; 1995-226291/30.  |   |       |
| XX               | P-PsDB; AAR75844.   |   |       |
| PT               | Isolated protein p140 polypeptide - and treatment of diabetes based |   |       |
| XX               | on tyrosine phosphorylation of protein p140.                        |   |       |
| PS               | Example; Page 28-33; 42pp; English.                                 |   |       |





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Qy 1012 GGCAGAGAGACTGCTCTACAAACATCATCTGCAGAGCT-----GTGAC 1056  
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Page 28

|    |      |   |      |
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| OY | 2794 | ATGATGATGAGCAGCATATTCGCGGTTGGGGTGGGTCACGTTGGCGTGGGACACAGAAAAATC | 2853 |
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| Db | 2863 | ATGCTCTGCAAGATCTCTGCAAGATCTCGGGTCACTTTGCGCGACACAGAAAGAGTC       | 2922 |
|    |      |   |      |
| OY | 2854 | CTGAAACACTATCAGCGTGAACGGGGCGGAGTAACACAACTTCAGTCTGTGGAGTTGA      | 2913 |
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Search completed: July 10, 2001, 18:40:55  
Job time: 6512 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 16:06:53 ; Search time 86.52 Seconds

(without alignments)  
6342.362 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962 1 CTGCTCGCCGCGTGAGAGA.....CCAGCCCGCCCTCTGC 2962

Sequence: IDENTITY\_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/1na/PCtus.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/1na/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description       |
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| 1          | 2962   | 100.0       | 2962   | 2     | US-08-449-645A-10 |
| 2          | 2962   | 100.0       | 2962   | 2     | US-08-702-367A-10 |
| 3          | 2962   | 100.0       | 2962   | 5     | PCT-US95-04681-10 |
| 4          | 2498   | 84.3        | 3105   | 4     | US-08-542-635-1   |
| 5          | 2185.6 | 73.8        | 4049   | 1     | US-08-162-809-17  |
| 6          | 2187.6 | 71.8        | 4097   | 1     | US-08-162-809-11  |
| 7          | 1581.6 | 53.4        | 3546   | 1     | US-08-162-809-9   |
| 8          | 1543.4 | 52.1        | 3591   | 1     | US-08-162-809-13  |
| 9          | 1526.4 | 51.5        | 4027   | 1     | US-08-348-143-3   |
| 10         | 1526.4 | 51.5        | 4027   | 1     | US-08-348-143-4   |
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| 12         | 1526.4 | 51.5        | 4027   | 1     | US-08-571-785-4   |
| 13         | 1520.8 | 51.3        | 2982   | 1     | US-08-348-143-2   |
| 14         | 1520.8 | 51.3        | 2982   | 1     | US-08-571-785-2   |
| 15         | 1459.6 | 49.6        | 3133   | 1     | US-08-162-809-1   |
| 16         | 1196.8 | 40.4        | 3776   | 1     | US-08-162-809-7   |
| 17         | 1075   | 36.3        | 3969   | 1     | US-08-436-044-5   |
| 18         | 1075   | 36.3        | 3969   | 1     | US-08-222-616-23  |
| 19         | 1075   | 36.3        | 3969   | 1     | US-08-436-054-5   |
| 20         | 1075   | 36.3        | 3969   | 5     | PCT-US95-04228-23 |
| 21         | 1075   | 36.3        | 3969   | 5     | PCT-US95-08812-5  |
| 22         | 1037.2 | 35.0        | 3116   | 2     | US-08-449-645A-14 |
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| 24         | 1035.6 | 35.0        | 3348   | 5     | US-08-222-616-34  |
| 25         | 1035.6 | 35.0        | 3348   | 5     | PCT-US95-04228-34 |
| 26         | 1035.6 | 35.0        | 3348   | 5     | US-08-162-809-15  |
| 27         | 992.8  | 33.5        | 3254   | 1     | US-08-162-809-15  |

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|----|-------|------|------|---|--------------------|-------------------|
| 28 | 956.8 | 32.3 | 3162 | 2 | US-08-449-645A-12  | Sequence 12, Appl |
| 29 | 956.8 | 32.3 | 3162 | 5 | PCT-US95-04681-12  | Sequence 12, Appl |
| 30 | 956.8 | 32.3 | 3162 | 5 | PCT-US95-04681-12  | Sequence 12, Appl |
| 31 | 949.4 | 32.1 | 2820 | 1 | US-08-162-809-5    | Sequence 5, Appl1 |
| 32 | 943.8 | 31.9 | 4304 | 5 | PCT-US96-00419-1   | Sequence 1, Appl1 |
| 33 | 909.6 | 30.7 | 3132 | 1 | US-08-167-919A-9   | Sequence 9, Appl1 |
| 34 | 909.6 | 30.7 | 3132 | 3 | US-08-715-106-9    | Sequence 9, Appl1 |
| 35 | 907   | 30.6 | 4529 | 2 | US-08-449-645A-16  | Sequence 16, Appl |
| 36 | 907   | 30.6 | 4529 | 2 | US-08-702-367A-16  | Sequence 16, Appl |
| 37 | 907   | 30.6 | 4529 | 5 | PCT-US95-04681-16  | Sequence 16, Appl |
| 38 | 869   | 29.3 | 3906 | 2 | US-08-469-537A-102 | Sequence 102, App |
| 39 | 697.2 | 23.5 | 3592 | 2 | US-08-162-809-3    | Sequence 100, App |
| 40 | 661.2 | 22.3 | 3059 | 1 | US-08-162-809-21   | Sequence 3, Appl1 |
| 41 | 628.6 | 21.3 | 3056 | 1 | US-08-162-809-19   | Sequence 21, Appl |
| 42 | 605.2 | 20.4 | 3125 | 1 | US-08-442-248-1    | Sequence 19, Appl |
| 43 | 572.8 | 19.3 | 4165 | 1 | US-08-440-815-1    | Sequence 1, Appl1 |
| 44 | 572.8 | 19.3 | 4165 | 1 | US-08-440-815-1    | Sequence 1, Appl1 |
| 45 | 564   | 19.0 | 4322 | 1 | US-08-673-789-1    | Sequence 1, Appl1 |

## ALIGNMENTS

RESULT 1  
US-08-449-645A-10  
; Sequence 10, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Amgen Patent Operations/RBM  
; STREET: 1840 DeWitt Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,645A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2962 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2913  
; US-08-449-645A-10

Query Match 100.0%; Score 2962; DB 2; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGCTCGCCGCGTGAGAGAAGCGTAAATGACTCCACTACAGCAGCTGAGCTGGGC 60  
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OY 361 TGGGTGAAGTGGATACCATTTGACCGACGAGAGCTTTCACAGTGGACCTGGGTGGC 420  
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Db 421 CGCGTCAATGAATAACAACACGAGTGGAGCTTGGACCTGTGTCGCGACGCGCTTC 480  
OY 481 TACTGGGCTTCAGAGACTATGGGGGCTGATGCCCTCATGCCCGCGCTGCTTCTAC 540  
Db 481 TACTGGGCTTCAGAGACTATGGGGGCTGATGCCCTCATGCCCGCGCTGCTTCTAC 540  
OY 541 CGCAAGTGGCCCCCGCATCATCAAGATGGCGCATCTTCAGAGAAACCTGTGGGGGCT 600  
Db 541 CGCAAGTGGCCCCCGCATCATCAAGATGGCGCATCTTCAGAGAAACCTGTGGGGGCT 600  
OY 601 GAGAGACATCGTGGTGGCTGCCCGGGGAGTGCATGCGCCATGCGGAAGAGTGGAT 660  
Db 601 GAGAGACATCGTGGTGGCTGCCCGGGGAGTGCATGCGCCATGCGGAAGAGTGGAT 660  
OY 661 GTACCCATCAAGCTCTACTGTAAAGGGGAGGGGAGTGGGTGGGCCATCGGGGCGCTG 720  
Db 661 GTACCCATCAAGCTCTACTGTAAAGGGGAGGGGAGTGGGTGGGCCATCGGGGCGCTG 720  
OY 721 ATGTGCAAGACAGGCTTGAAGGCGCTTGAGAAATGGACCGCTGCGGAGGTTGTCAATCT 780  
Db 721 ATGTGCAAGACAGGCTTGAAGGCGCTTGAGAAATGGACCGCTGCGGAGGTTGTCAATCT 780  
OY 781 GGGACTTTCAAGGCGCAACCAAGGGGATGAGGCGTGTACCCACTGCTCCATCAACAGCGG 840  
Db 781 GGGACTTTCAAGGCGCAACCAAGGGGATGAGGCGTGTACCCACTGCTCCATCAACAGCGG 840  
OY 841 ACCACTTTCGAAGGGGCGACCAACTGTGTGCGCAATGGCTACTACATAGAGAGACCTG 900  
Db 841 ACCACTTTCGAAGGGGCGACCAACTGTGTGCGCAATGGCTACTACATAGAGAGACCTG 900  
OY 901 GACCCCTCGACATGCGCTGCAACCAATCCCTCGCGCGCCAGGCTGTGATTTCCAGT 960  
Db 901 GACCCCTCGACATGCGCTGCAACCAATCCCTCGCGCGCCAGGCTGTGATTTCCAGT 960  
OY 961 GTCAATGAACCTCCCTCATGTGTGAGTGAACCCCTCCCGCGACTCCGAGGCGGAGAG 1020  
Db 961 GTCAATGAACCTCCCTCATGTGTGAGTGAACCCCTCCCGCGACTCCGAGGCGGAGAG 1020  
OY 1021 GACCTGCTTACACATCAATCTGCAAGAGCTGTGGGCGGGGGGCTGCTACACCGC 1080  
Db 1021 GACCTGCTTACACATCAATCTGCAAGAGCTGTGGGCGGGGGGCTGCTACACCGC 1080  
OY 1081 TCGGGGGAATGTACAGTACGACGACGACGCTGAGGCTGTGACGACGACGACATTTAC 1140  
Db 1081 TCGGGGGAATGTACAGTACGACGACGACGCTGAGGCTGTGACGACGACGACATTTAC 1140  
OY 1141 ATCAGTACCTGTGGCGACACACGACGATACCTTGGAGATCCAGGCTGTGAAGGCGCTT 1200  
Db 1141 ATCAGTACCTGTGGCGCGACACGACGATACCTTGGAGATCCAGGCTGTGAAGGCGCTT 1200

Db 1141 ATCAGTACCTGTGGCGCGACACGACGATACCTTGCAGATCCAGGCTGTGAAGGCGCTT 1200  
OY 1201 ACTGACGAGAGCCCTTCCTGCGCTCAATGTCCTGTGAAACATCCACCAACGAGGCA 1260  
Db 1201 ACTGACGAGAGCCCTTCCTGCGCTCAATGTCCTGTGAAACATCCACCAACGAGGCA 1260  
OY 1261 GCTTCATCGGCAATGTTCATCATGATCAGTGAAGCGGACCGCTGACACATTTACCTG 1320  
Db 1261 GCTTCATCGGCAATGTTCATCATGATCAGTGAAGCGGACCGGACCGGACACATTTACCTG 1320  
OY 1321 TCGTGGTCCAGCGCGACGACCGCCATGCGGTGATCTGCAATGAGTGCAGTACTAT 1380  
Db 1321 TCGTGGTCCAGCGCGCGACGACCGCCATGCGGTGATCTGCAATGAGTGCAGTACTAT 1380  
OY 1381 GAGAGAGGCTCAGTGTCAACGGCGACGACGACGACGACGACGACGACGACGACGACG 1440  
Db 1381 GAGAGAGGCTCAGTGTCAACGGCGACGACGACGACGACGACGACGACGACGACGACG 1440  
OY 1441 GGCCTCAAGCGCGCGCATCTATGCTTTCAGAGTGGGCGACGACGACGACGACGACG 1500  
Db 1441 GGCCTCAAGCGCGCGCATCTATGCTTTCAGAGTGGGCGACGACGACGACGACGACG 1500  
OY 1501 GGGGCTTACAGCGCGCAAGATGATCTTCAGACATGACAGACGACGACGACGACGACG 1560  
Db 1501 GGGGCTTACAGCGCGCAAGATGATCTTCAGACATGACAGACGACGACGACGACGACG 1560  
OY 1561 ATCCAGGAGAGTTCACACTCATGCGGCTGCGCGCGCTGCGGCTGCTTCTCAT 1620  
Db 1561 ATCCAGGAGAGTTCACACTCATGCGGCTGCGCGCGCTGCGGCTGCTTCTCAT 1620  
OY 1621 GCTGTGGTGTCAATCGCCATCGTGTGTAAACAGAGGGGGTTTGAAGCGTGTGACTCGGAG 1680  
Db 1621 GCTGTGGTGTCAATCGCCATCGTGTGTAAACAGAGGGGGTTTGAAGCGTGTGACTCGGAG 1680  
OY 1681 TACAGGACAGCTGCAACACTACACAGTGGCCACATTAACCCAGGACATGAAGATCTAC 1740  
Db 1681 TACAGGACAGCTGCAACACTACACAGTGGCCACATTAACCCAGGACATGAAGATCTAC 1740  
OY 1741 ATCGATCCTTTCACATGAGGAGCGCCCAAGGAGTGGGGAGTTTGCAGAGAAAT 1800  
Db 1741 ATCGATCCTTTCACATGAGGAGCGCCCAAGGAGTGGGGAGTTTGCAGAGAAAT 1800  
OY 1801 GACATCTCTGTGTCAAAATTTGAGCAGGTGATCGAGCAGGGAGTTTGGCAGGCTGCG 1860  
Db 1801 GACATCTCTGTGTCAAAATTTGAGCAGGTGATCGAGCAGGGAGTTTGGCAGGCTGCG 1860  
OY 1861 AGTGGCCACTGTAAGTGTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAGAGGCTCAAG 1920  
Db 1861 AGTGGCCACTGTAAGTGTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAGAGGCTCAAG 1920  
OY 1921 TCGGGCTACAGGAGGAGGCGCGCGGACTTCTGAGGCAACCTTCATCATGGGCGAG 1980  
Db 1921 TCGGGCTACAGGAGGAGGCGCGCGGACTTCTGAGGCAACCTTCATCATGGGCGAG 1980  
OY 1981 TTCGACCATCCCAACGTCATCCACTGGAAGGTGTGCTGCAAGAGACACACCTGTGAT 2040  
Db 1981 TTCGACCATCCCAACGTCATCCACTGGAAGGTGTGCTGCAAGAGACACACCTGTGAT 2040  
OY 2041 ATCATCAGGAGTTCATGGAATGCTCCCTGAGCTCTTTCTCCGGCAAAACGATGGG 2100  
Db 2041 ATCATCAGGAGTTCATGGAATGCTCCCTGAGCTCTTTCTCCGGCAAAACGATGGG 2100  
OY 2101 CAGTTCAGGATCCAGGCTGGGCGATGCTTCGGGGGCAATGCACTGGCATGAAGTAC 2160  
Db 2101 CAGTTCAGGATCCAGGCTGGGCGATGCTTCGGGGGCAATGCACTGGCATGAAGTAC 2160  
OY 2161 CTGGGACATGAACTATGTTACCGTGAACCTGGCTGGCGCAACATCTCTGCAACAGC 2220  
Db 2161 CTGGGACATGAACTATGTTACCGTGAACCTGGCTGGCGCAACATCTCTGCAACAGC 2220  
OY 2221 AACCTGCTGCAAGGTGTGCGACTTTGGGCTTCACGCTTCTAGAGGACGATACCTCA 2280  
Db 2221 AACCTGCTGCAAGGTGTGCGACTTTGGGCTTCACGCTTCTAGAGGACGATACCTCA 2280

Oy 2281 GACCCACCTACACAGTGGCCCTGGGCGGAAAGTTCCCATCCGCTGGACAGACCCCGAA 2340  
|||  
Db 2281 GACCCACCTACACAGTGGCCCTGGGCGGAAAGTTCCCATCCGCTGGACAGACCCCGAA 2340  
Oy 2341 GGCATCGATACCGGAACTTACCTCGGCGCATGTATGTGTAGCTAGCGCATTTGTCAAG 2400  
|||  
Db 2341 GGCATCGATACCGGAACTTACCTCGGCGCATGTATGTGTAGCTAGCGCATTTGTCAAG 2400  
Oy 2401 TGGAGGTGATGTCTATGTGGGAGGCGCCCTACTGTGGACATGACCAACAGAGTATATC 2460  
|||  
Db 2401 TGGAGGTGATGTCTATGTGGGAGGCGCCCTACTGTGGACATGACCAACAGAGTATATC 2460  
Oy 2461 AATGCCATTGAGCAGAGCATATCGGCTGCCACCGCCCATGAGACTGCCCGACGCCCTGCAC 2520  
|||  
Db 2461 AATGCCATTGAGCAGAGCATATCGGCTGCCACCGCCCATGAGACTGCCCGACGCCCTGCAC 2520  
Oy 2521 CAACATCATGTGAGTGTGGCAGAGGACCGCAACACCGGCCCAACATGTGGCGCAAT 2580  
|||  
Db 2521 CAACATCATGTGAGTGTGGCAGAGGACCGCAACACCGGCCCAACATGTGGCGCAAT 2580  
Oy 2581 GTCAACAGCTAGACAAATGATCGGCAATCCCAACAGCTCAAAAGCCATGGCGCCCTC 2640  
|||  
Db 2581 GTCAACAGCTAGACAAATGATCGGCAATCCCAACAGCTCAAAAGCCATGGCGCCCTC 2640  
Oy 2641 TCCTCTGGCATCAACCTGCGCTGTGGACCGCACGATCCCGACTACACAGCTTTAAC 2700  
|||  
Db 2641 TCCTCTGGCATCAACCTGCGCTGTGGACCGCACGATCCCGACTACACAGCTTTAAC 2700  
Oy 2701 ACGGTGACAGATGGCTGGAGGCGCATCAAGATGGGCGAGTCAAGAGAGATGTGCCCAAT 2760  
|||  
Db 2701 ACGGTGACAGATGGCTGGAGGCGCATCAAGATGGGCGAGTCAAGAGAGATGTGCCCAAT 2760  
Oy 2761 GCCGCTTACCTCTTGTAGCTGTCTCTAGATGATGAGAGATTTCTCCGGGTT 2820  
|||  
Db 2761 GCCGCTTACCTCTTGTAGCTGTCTCTAGATGATGAGAGATTTCTCCGGGTT 2820  
Oy 2821 GGGGTCTACTTGGCTGGCCACCAAGAAAAATCTGAAACAGTATCCAGTGTGCGGCG 2880  
|||  
Db 2821 GGGGTCTACTTGGCTGGCCACCAAGAAAAATCTGAAACAGTATCCAGTGTGCGGCG 2880  
Oy 2881 CAGATGAACCAAGATTCAGTGTGTGGAGTTTGACATTCACCTGCTCCGCTACCTCTTC 2940  
|||  
Db 2881 CAGATGAACCAAGATTCAGTGTGTGGAGTTTGACATTCACCTGCTCCGCTACCTCTTC 2940  
Oy 2941 CTCCAAGCCCGCCCTCTCTGC 2962  
|||  
Db 2941 CTCCAAGCCCGCCCTCTCTGC 2962

RESULT 2  
US-08-702-367A-10  
; Sequence 10, Application US/08702367A  
; Patent No. 5981246  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702.367A

;; FILING DATE: 435  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winer, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-287  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2962 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..2913  
;; US-08-702-367A-10  
  
Query Match 100.0%; Score 2962; DB 2; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 CTGCTCGCCGCGGTGAGAGAAAGCTTAATGAGTCTACAGAGCTGTAGCTGGGC 60  
|||  
Db 1 CTGCTCGCCGCGGTGAGAGAAAGCTTAATGAGTCTACAGAGCTGTAGCTGGGC 60  
Oy 61 TGGATGTGATCTCTCATCATGAGGTGGAGAGAGTGTAGTGTAGATGAGAACATGAA 120  
|||  
Db 61 TGGATGTGATCTCTCATCATGAGGTGGAGAGAGTGTAGTGTAGATGAGAACATGAA 120  
Oy 121 ACGATCCGACGTACAGAGTGTGCAAGTGTGTAGTCAAGCACAACAGCTGGCTAGG 180  
|||  
Db 121 ACGATCCGACGTACAGAGTGTGCAAGTGTGTAGTCAAGCACAACAGCTGGCTAGG 180  
Oy 181 ACCAAGTTATCCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGAATTTTCGGTG 240  
|||  
Db 181 ACCAAGTTATCCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGAATTTTCGGTG 240  
Oy 241 ACCTGCTGACAGATCCCGAGCTGTGCTGCTGCTGCAAGAGACCTTCAACCTTAT 300  
|||  
Db 241 ACCTGCTGACAGATCCCGAGCTGTGCTGCTGCTGCTGCAAGAGACCTTCAACCTTAT 300  
Oy 301 TACTATGAGGCTGATTTGATCTGCGGCAACAGACCTTCCCACTGGATGAGAACCA 360  
|||  
Db 301 TACTATGAGGCTGATTTGATCTGCGGCAACAGACCTTCCCACTGGATGAGAACCA 360  
Oy 361 TGGGTGAAGTGTGATACATTGACAGCCGAGAGACTTCTCCAGGTGAGCTGGTGGC 420  
|||  
Db 361 TGGGTGAAGTGTGATACATTGACAGCCGAGAGACTTCTCCAGGTGAGCTGGTGGC 420  
Oy 421 CGGTCATGAAATCAACACGAGGTGGGAGCTTGGACCTGTCCGACAGCGCTTC 480  
|||  
Db 421 CGGTCATGAAATCAACACGAGGTGGGAGCTTGGACCTGTCCGACAGCGCTTC 480  
Oy 481 TACCTGGCTTCCAGAGATGAGGCGGTGATGTCCCTCATGCGGTGCTTCTTAC 540  
|||  
Db 481 TACCTGGCTTCCAGAGATGAGGCGGTGATGTCCCTCATGCGGTGCTTCTTAC 540  
Oy 541 CGCAAGTGGCCCGCATATCCAGAAATGAGGCTTCCAGAAACCTGTGCGGGGCT 600  
|||  
Db 541 CGCAAGTGGCCCGCATATCCAGAAATGAGGCTTCCAGAAACCTGTGCGGGGCT 600  
Oy 601 GAGACACATCGCTGTGTGCTCCCGGGGACAGTGCATGCCAATGCGGAAAGGTGAT 660  
|||  
Db 601 GAGACACATCGCTGTGTGCTCCCGGGGACAGTGCATGCCAATGCGGAAAGGTGAT 660  
Oy 661 GTACCATCAAGCTTACTGTAAAGGAGGAGCGAGTGTGCTGCTGCTGCTGCTGCT 720  
|||  
Db 661 GTACCATCAAGCTTACTGTAAAGGAGGAGCGAGTGTGCTGCTGCTGCTGCTGCT 720  
Oy 721 ATGTCAAAAGCAGGCTTGAAGGCGGTGGAATGACACCGTCTGCGAGGTTGTCACT 780  
|||  
Db 721 ATGTCAAAAGCAGGCTTGAAGGCGGTGGAATGACACCGTCTGCGAGGTTGTCACT 780

|    |      |   |      |
|----|------|---|------|
| QY | 781  | GGGACTTTCAAAGGCGCAACCAAGGGGGATGAGCGCTGTACCCACTGCTGCTCCATCAACAGCCGG  | 840  |
| Db | 781  | GGGACTTTCAAAGGGCGCAACCAAGGGGGATGAGCGCTGTACCCACTGCTGCTCCATCAACAGCCGG | 840  |
| QY | 841  | ACCACTTGTGAAGGGGCGACCAACTGTGTGTGGCGGAATGGGCTACTACAGACACCGTG         | 900  |
| Db | 841  | ACCACTTGTGAAGGGGCGCACCAACTGTGTGTGGCGGAATGGGCTACTACAGACACACCTG       | 900  |
| QY | 901  | GACCCCTTGACATGCCCCGTGCACACCATCCCTCGCGGCCCCAGGCTGTGATTTCCAGT         | 960  |
| Db | 901  | GACCCCTTGACATGCCCCGTGCACACCATCCCTCGCGGCCCCAGGCTGTGATTTCCAGT         | 960  |
| QY | 961  | GTCAATGTGAGACTCCCTCCATGCTGGAGTGGAGACCCCTCCCGGAGACTCGGAGGCCGAGAG     | 1020 |
| Db | 961  | GTCAATGTGAGACTCCCTCCATGCTGGAGTGGAGACCCCTCCCGGAGACTCGGAGGCCGAGAG     | 1020 |
| QY | 1021 | GACCTGCTCTCAACATCATCTGCAAGAGTGTGGCTCGGAGCGGGGCTGCTGTGACCCGC         | 1080 |
| Db | 1021 | GACCTGCTCTCAACATCATCTGCAAGAGTGTGGCTCGGAGCGGGGCTGCTGTGACCCGC         | 1080 |
| QY | 1081 | TGGCGGGACATGTACAGGTACGCAACCGCGCACTTGGCTGTACCGAGGCACGCCATTTAC        | 1140 |
| Db | 1081 | TGGCGGGACATGTACAGGTACGCAACCGCGCACTTGGCTGTACCGAGGCACGCCATTTAC        | 1140 |
| QY | 1141 | ATCAGTGCATGCTGTGGCCCGCACACCGACATACCTTGAGATGCAGGCTGTGAACGGCGCTT      | 1200 |
| Db | 1141 | ATCAGTGCATGCTGTGGCCCGCACACCGACATACCTTGAGATGCAGGCTGTGAACGGCGCTT      | 1200 |
| QY | 1201 | ACTGCACAGAGCCCCCTTCTGCGCTCAAGTTCGCTGTGTAACATCACACCAACCGAGCA         | 1260 |
| Db | 1201 | ACTGCACAGAGCCCCCTTCTGCGCTCAAGTTCGCTGTGTAACATCACACCAACCGAGCA         | 1260 |
| QY | 1261 | GCTCCATCGGGAGGTGCATCATATGACATCAGGTGAGCGGACCGTGGACGATTAACCGTG        | 1320 |
| Db | 1261 | GCTCCATCGGGAGGTGCATCATATGACATCAGGTGAGCGGACCGTGGACGATTAACCGTG        | 1320 |
| QY | 1321 | TCGTGTGCCAGCCGGAGCCAGCCCCAATGGCGTGATCCTGAGCATATGAGTGCAGTACTAT       | 1380 |
| Db | 1321 | TCGTGTGCCAGCCGGAGCCAGCCCCAATGGCGTGATCCTGAGCATATGAGTGCAGTACTAT       | 1380 |
| QY | 1381 | GAGAAAGAGCTCACTGATGATCAACGCCACACGCATATAAAAGGCCCCACCAACAGGTCAAG      | 1440 |
| Db | 1381 | GAGAAAGAGCTCACTGATGATCAACGCCACACGCATATAAAAGGCCCCACCAACAGGTCAAG      | 1440 |
| QY | 1441 | GGCCTCAAAAGCCGGCGGCATCTATGTCTTCACAGTGCGGGACGCACTGTGGCAGGCTAC        | 1500 |
| Db | 1441 | GGCCTCAAAAGCCGGCGGCATCTATGTCTTCACAGTGCGGGACGCACTGTGGCAGGCTAC        | 1500 |
| QY | 1501 | GGGCGCTACAGCGGCGAAGATGTACTTCCAGACCATGACAGAAAGCCGAGTACAGCAAGC        | 1560 |
| Db | 1501 | GGGCGCTACAGCGGCGAAGATGTACTTCCAGACCATGACAGAAAGCCGAGTACAGCAAGC        | 1560 |
| QY | 1561 | ATTCAGAGGGAAGTGGCCATCATCATCGGCTCTCGGCCGCGGCGCTGGTCTCTCTCATTT        | 1620 |
| Db | 1561 | ATTCAGAGGGAAGTGGCCATCATCATCGGCTCTCGGCCGCGGCGCTGGTCTCTCTCATTT        | 1620 |
| QY | 1621 | GCTGTGGTGTGCATCGCCATCGTGTGTAAACAGAGGGGGTTTGAACGCTGCTGACTCGAG        | 1680 |
| Db | 1621 | GCTGTGGTGTGCATCGCCATCGTGTGTAAACAGAGGGGGTTTGAACGCTGCTGACTCGAG        | 1680 |
| QY | 1681 | TACACGGACAAAGCTGCAACACTACACCACTAGGCGCATATAACCCAGGCGATGAAGTCTAC      | 1740 |
| Db | 1681 | TACACGGACAAAGCTGCAACACTACACCACTAGGCGCATATAACCCAGGCGATGAAGTCTAC      | 1740 |
| QY | 1741 | ATCAGATCCTTTCACCTTACGAGAGACCCCAACGAGAGCAAGTGCGGGATTTGGCAAGAAATTT    | 1800 |
| Db | 1741 | ATCAGATCCTTTCACCTTTCACGAGAGACCCCAACGAGAGCAAGTGCGGGATTTGGCAAGAAATTT  | 1800 |
| QY | 1801 | GACATCTCTCTGTGTCAAAATTTGACAGGTGATGAGCAGGGGAGCTTTGGCGAGCTGCG         | 1860 |
| Db | 1801 | GACATCTCTCTGTGTCAAAATTTGACAGGTGATGAGCAGGGGAGCTTTGGCGAGCTGCG         | 1860 |

|    |      |  |      |
|----|------|--|------|
| QY | 1861 | AGTGGCACCTGTAAGCTGCCAGGCAAGAGAGAAATCTTTGTGGCATCAAGCCTCAAG        | 1920 |
| Db | 1861 | ACTGGCCACCTGAAGCTGCCAGGCAAGAGAGAAATCTTTGTGGCATCAAGCCTCAAG        | 1920 |
| QY | 1921 | TGGGCTACAGGGGAAGACAGCGCGGGACTTCTCTAGCGAAGCCCTCATCTATGGCCAG       | 1980 |
| Db | 1921 | TGGGCTACAGGGGAAGACAGCGCGGGACTTCTCTAGCGAAGCCCTCATCTATGGCCAG       | 1980 |
| QY | 1981 | TTTGCACATCCCAACGTGATCCACCTGGAGGGTGTGTAACCAAGACACACCTGTGATG       | 2040 |
| Db | 1981 | TTTGCACATCCCAACGTGATCCACCTGGAGGGTGTGTAACCAAGACACACCTGTGATG       | 2040 |
| QY | 2041 | ATCATACACCGAGTTCAATGGAAGAAATGGCTCCCTGACATCTTCTCTCGGCAAAACATATGG  | 2100 |
| Db | 2041 | ATCATACACCGAGTTCAATGGAAGAAATGGCTCCCTGACATCTTCTCTCGGCAAAACATATGG  | 2100 |
| QY | 2101 | CAGTTCACAGTCATCCAGCTGGTGGGCAATCTTCCGGGGATGGACGTGGCATGAATGATC     | 2160 |
| Db | 2101 | CAGTTCACAGTCATCCAGCTGGTGGGCAATCTTCCGGGGATGGACGTGGCATGAATGATC     | 2160 |
| QY | 2161 | CTGGCAGACATGAACTATATGTTCAACCGTGACCTGGCTGCCCGCAACATCTCTGTCATACAGC | 2220 |
| Db | 2161 | CTGGCAGACATGAACTATATGTTCAACCGTGACCTGGCTGCCCGCAACATCTCTGTCATACAGC | 2220 |
| QY | 2221 | AACTGTGCTCTCAAGAGTGTGGACTTTGGGCTCTACAGCTTTCTTAGAGAGAGATACCTCA    | 2280 |
| Db | 2221 | AACTGTGCTCTCAAGAGTGTGGACTTTGGGCTCTACAGCTTTCTTAGAGAGAGATACCTCA    | 2280 |
| QY | 2281 | GACCCCACTACACACTGGCCCTGGGGGGAAATTCGCCATCGCTGGGAGACGCCCGGAA       | 2340 |
| Db | 2281 | GACCCCACTACACACTGGCCCTGGGGGGAAATTCGCCATCGCTGGGAGACGCCCGGAA       | 2340 |
| QY | 2341 | GCCATCCAGTACCCGGAAGTTTACCTCGCGCCAGTGAATGTGGAGCTACGGCATTTGTATG    | 2400 |
| Db | 2341 | GCCATCCAGTACCCGGAAGTTTACCTCGCGCCAGTGAATGTGGAGCTACGGCATTTGTATG    | 2400 |
| QY | 2401 | TGGGAGGTGATGTCTATATGGGGAAGCGCCCTACTGGGACATGACACACAGATGTAACT      | 2460 |
| Db | 2401 | TGGGAGGTGATGTCTATATGGGGAAGCGCCCTACTGGGACATGACACACAGATGTAACT      | 2460 |
| QY | 2461 | AATGCGAATTAGACAGACATATGGGCTGGCCACGCGCCATGGACTGGCCGAGGCCCTGTGAC   | 2520 |
| Db | 2461 | AATGCGAATTAGACAGACATATGGGCTGGCCACGCGCCATGGACTGGCCGAGGCCCTGTGAC   | 2520 |
| QY | 2521 | CAACTCATGTGCGACTTTTGGCAAGAGACCGCAACACCGGCCCAAGTTGGGCGCAAAAT      | 2580 |
| Db | 2521 | CAACTCATGTGCGACTTTTGGCAAGAGACCGCAACACCGGCCCAAGTTGGGCGCAAAAT      | 2580 |
| QY | 2581 | GTCAACACGCTAGAATAAGATGATCCGCAATCCCAACAGCCTCAAGGCCATGGCGCCCTC     | 2640 |
| Db | 2581 | GTCAACACGCTAGAATAAGATGATCCGCAATCCCAACAGCCTCAAGGCCATGGCGCCCTC     | 2640 |
| QY | 2641 | TTCTCTGGCATCAATCTGGCGCTGTCTGGACCGCAGCATGCCGACTACACACGCTTTAAC     | 2700 |
| Db | 2641 | TTCTCTGGCATCAATCTGGCGCTGTCTGGACCGCAGCATGCCGACTACACACGCTTTAAC     | 2700 |
| QY | 2701 | ACGGGGACGAGTGGCTGGAGGGCCATCAAGATGGGGCACTAACAGAGAGCTTGGCCAAAT     | 2760 |
| Db | 2701 | ACGGGGACGAGTGGCTGGAGGGCCATCAAGATGGGGCACTAACAGAGAGAGCTTGGCCAAAT   | 2760 |
| QY | 2761 | GCGGCGCTTCACTCTTTTGAAGCTGTCTCAGATGATGATGGAGACATTTCTCGGGATT       | 2820 |
| Db | 2761 | GCGGCGCTTCACTCTTTTGAAGCTGTCTCAGATGATGATGGAGACATTTCTCGGGATT       | 2820 |
| QY | 2821 | GGGGTCACTTTGGCTGGCCACCGAAGAAAAAATCTGAAACAGTATCAAGTATCGGGCG       | 2880 |
| Db | 2821 | GGGGTCACTTTGGCTGGCCACCGAAGAAAAAATCTGAAACAGTATCAAGTATCGGGCG       | 2880 |
| QY | 2881 | CAGATGAACAGATTCAGTGTGGGAGGTTTACATTCACCTGCGCTGGGCTCACCTCTTC       | 2940 |
| Db | 2881 | CAGATGAACAGATTCAGTGTGGGAGGTTTACATTCACCTGCGCTGGGCTCACCTCTTC       | 2940 |
| QY | 2941 | CTTCAAGCCCCGCCCTCTGC   | 2992 |

Db 2941 CTCACAGCCCCGCCCCCTGTC 2962

RESULT 3

PCT-US95-04681-10

Sequence 10, Application PC/TUS9504681

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04681

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2962 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2913

PCT-US95-04681-10

Query Match 100.0%; Score 2962; DB 5; Length 2962;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTCCGCCCCCGTGGAAAGAAAGCTTAATGACATCCACTACAGGACTGCTGAGCTGGC 60  
Db 1 CTGCTCCGCCCGTGGAAAGAAAGCTTAATGACATCCACTACAGGACTGCTGAGCTGGC 60  
QY 61 TGGATGGTGCATCTCCATCAGAGGTGGGAAGAGTGAAGTGCATGAGTAACATGAAAC 120  
Db 61 TGGATGGTGCATCTCCATCAGAGGTGGGAAGAGTGAAGTGCATGAGTAACATGAAAC 120  
QY 121 AGCATCCGACGTAACAGAGTGTGCAACGCTTTGAGTCAAGCCAGAACTGGCTACGG 180  
Db 121 AGCATCCGACGTAACAGAGTGTGCAACGCTTTGAGTCAAGCCAGAACTGGCTACGG 180  
QY 181 ACCAAGTTATCCGGGGCGGTGGGGCCCGACCGATCCAGCTGGAGATGAAGTTTTCGGTG 240  
Db 181 ACCAAGTTATCCGGGGCGGTGGGGCCCGACCGATCCAGCTGGAGATGAAGTTTTCGGTG 240  
QY 241 CGTGACTGACAGCATCCCGACGCTGCTGCTGCTGCAAGAGAGACTTCAACCTCTAT 300  
Db 241 CGTGACTGACAGCATCCCGACGCTGCTGCTGCTGCAAGAGAGACTTCAACCTCTAT 300  
QY 301 TACTATGAGGCTGACTTTGACTGAGTGGCCACCAAGACTTCCCAACTGATGAGAAATCCA 360  
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QY 601 GAGAGCAATGCGTGGTGGCTGGCGGGGACGCTGATCCGCAATGGGGAAGAGTGGAT 660  
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Db 661 GTACCCATCAAGCTCTACTGTAAAGGGGACGCGAGTGGTGGTGGTGGTGGTGGTGG 720  
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QY 2701 ACGGTGAGAGTGGCTGTGAAGGCTATCAAGATGGGACATACAAAGAGAGCTTCCGCAAT 2760  
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QY 2881 CAGATCAACCAATTCAGTGTGTGAAGTTTGAATTCACCTGCTGCTGCTTC 2940  
Db 2881 CAGATCAACCAATTCAGTGTGTGAAGTTTGAATTCACCTGCTGCTGCTTC 2940  
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Db 2941 CTCCAGCCCGCCGCTCTGC 2962

RESULT 4  
US-08-542-635-1  
; Sequence 1, Application: us/08542635  
; Patent No. 6218356  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; APPLICANT: Letwin, Kenneth  
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
; TITLE OF INVENTION: TYROSINE KINASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bereskin & Parr  
; STREET: 40 King Street West, Box 401  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,635  
; FILING DATE:  
; CLASSIFICATION: E00  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mediamid, Shona S.  
; REGISTRATION NUMBER: 38,798  
; REFERENCE/DOCKET NUMBER: 3153-162  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 364-1398  
; TELEX: 06-23115  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3105 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:



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: ORGANISM: Mus musculus
: DEVELOPMENTAL STAGE: Embryo
: IMMEDIATE SOURCE:
: LIBRARY: Lambda gt10 cDNA library
: CLONE: Combined PubRACE A2 and K2 AND cDNA clones
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: Distal end of chromosome 4
: MAP POSITION: near the and-1 mutation
: US-08-542-635-1

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Query Match      84.3%  Score 2498;  DB 4;  Length 3105;
Best Local Similarity 90.5%;  Pred. No. 0;
Matches 2679;  Conservative 0;  Mismatches 275;  Indels 6;  Gaps 1;

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OY 61 TGGATGTCGATCCTCATCAGAGGTGGGAAGAGTGAAGTGGCTAGCATGAACATGAAC 120
Db 127 TGGATGTCATATCCCATCAGAGGTGGGAAGAGTGAAGTGGCTAGCATGAACATGAAC 186
OY 121 AGCATCCGACAGTACAGAGTGTGCAAGCTGTTGAGTCAAGCCAGAACTGGCTAGGC 180
Db 187 ACTATCCGATCCTACAGAGTGTGCAAGCTGTTGAGTCAAGCCAGAACTGGCTAGGC 246
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Db 487 CGCGTATGAAATCAACACCGAGTGGGAGCTTGGAGCTGTTGCCGACGCGCTTC 546
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OY 721 ATGTGCAAGAGGCTTTCGAGGCGGTGAGAAATGGCAACGCGTCCGAGGTGGCTATCT 780
Db 787 ATGTGCAAGAGGCTTTCGAGGCGGTGAGAAATGGCAACGCGTCTGCGAGGTGGCTATCT 846
OY 781 GGGACTTTCAAGGCAACCAAGGAGTGAAGCTTACCCACTGTCCATCAACAGCGG 840
Db 847 GGAACCTTCAAGGCAACCAAGGAGTGAAGCTTACCCACTGTCCATCAACAGCGG 906
OY 841 ACACCTTCTGAAGGAGGAGCAGCACTGTGTGCTGGCGCAATGGCTACTACAGAGACCTG 900

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Db 967 GACCCCTGTGAGATGCTGCTGCAACCAATCCCTTCCGGGCGCCAGGCTGTGATTTCCAGC 1026
OY 961 GTCAATGAGACCTCCCTCATGTGTGAGTGGAGACCTCCCGCGAGCTCGGAGCGGAGAG 1020
Db 1027 GTCAAGAGACATCCCTCATGTGTGAGTGGAGACCTCCCGCGAGCTCGGAGCGGAGAG 1086
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OY 1141 ATCAATGACCTGTGCTGCTGCAACCAAGTACAGCTTTCAGATCCAGGGGTGTAAGCGGCTT 1200
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OY 1201 ACTGACCAAGACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1267 ACTGACCAAGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1326
OY 1261 GCTCATGCGGAGTGTCCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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Db 1387 TCGTGTGCTGCGGCGGACCAAGCCCAATGGGCTGATGCTGCTGCTGCTGCTGCTGCTG 1446
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Db 1447 GAGAAGGAGCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1506
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Db 1927 GTCTGAGTGGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1986
OY 1915 CTCAAGTGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1974
Db 1987 CTCAAGTGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2046

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OY 481 TACGTGGCGCTTCAGAGCATATGGCGGTCATGCCCTCATCGGCGGTGTCTTAC 540  
DB 556 TACGTGGCGCTTCAGAGCATATGGCGGTCATGCCCTCATCGGCGGTGTCTTAC 615  
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DB 616 CGCAAGTGGCGCGCATCATCCAGATGGCGCGCATCTTCAGAGAAACCTTCGGGGAGG 675  
OY 601 GAGACACATCGCTGTGGTGTGGTGGCGGAGCTGATGCCATATCCGAGAGAGTGCAT 660  
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DB 1756 GACTGTGATACGAGGACGACCTGCAACAGTGGCCACATTAACCTGAGTACAGAGAT 1815  
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DB 1816 AAGATTTATATGATCATTTTACCTACGAGAGATCCCAATGAGGCTGTCAAGGAATTTGCA 1875  
OY 1792 AAGGAATTTGACATCTCCTGTGTCAAAATTTAGCAGAGTATCGAGACGAGGAGTTTGC 1851  
DB 1876 AAGGAATTTGATATCTCTGTGTGAAATTTGACAGAGTGTATGGGCGAGGAGTTTGT 1935  
OY 1852 GAGGTCTGCACTGGCCACTGAGCTGCCAGGCAAGAGAGATCTTTGTGCCATCAG 1911  
DB 1936 GAGGTCTGCACTGGCCACTGCAACTCTCCGCAAAAGAGATCTTTGTGCCATCAG 1995  
OY 1912 ACGCTCAAGTGGGCTTACAGGAGAGAGAGCGCGGAGCTTCTGAGGAAAGCTCCATC 1971  
DB 1996 ACCCTGAAGTGTGTATACAGAGAGAGAGAGAGCGGAGCTTCTGAGGAAAGCAAGCTC 2055  
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DB 2116 CCAGTCAATGATCATACAGAGTTCATGAGAGATGAGCTGTTGAGCTCCTTCTGAGCA 2175  
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DB 2176 AATATGGGAGTTCACAGTTCATCAGCTGGTGGGAGTGTGGGCGATGAGAGCTGCG 2235  
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DB 2236 ATGAAGTACCTGGGAGTGAATATGTTCAACGCTGAGCTGGTGGCGGCAATCTCTC 2295  
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DB 2296 GTCAACAGCAACCTGTGTGCAAGGTGTGGACTTTGGGCTCTCTCGTTCTGAGAGAT 2355  
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DB 2476 ATTGTATGTGGAGGTGTATGTCTATGGGAGCGGCTTATGTGAGCATGACCAATCA 2535  
OY 2452 GATGTATCAATGCGATTGAGCAGAGTATTCGCTGTGACCGCCATATGAGTGGCCGAGC 2511  
DB 2536 GATGTATCAATGCGATTGAGCAGAGTATTCGCTGTGACCGCCATATGAGTGGCCGAGC 2595  
OY 2512 GCCCTGACCAACCTCATCTGAGCTGTGGCAGAGAGAGCAACGACCGGCCCAAGTCT 2571  
DB 2596 GCCCTGACCAACCTCATCTGAGCTGTGGCAGAGAGATGAGAAACCAACCAATTTT 2655  
OY 2572 GCGCAAAATTTGTCAACAGCTTACAGAGATGATCCGCAATCCCAACAGCTTCAAGCCATG 2631

|    |      |   |       |
|----|------|---|-------|
| Db | 2656 | GGACAGATTGTCAACACTTTAGCAAAATAGATCCGAATTCCTAATATGCTGAAGCCATG     | 271.5 |
| QY | 2632 | GGGCCCCCTCTCTCTGTGGCATCAACTGCGCTGTGTGGACCGCAGCATGCCGACTACACC    | 265.1 |
| Db | 2716 | GCACCTCTCCCTCTGGGGTTAACTCCCTCTACTTGACCGGCACATCCAGATTTATACC      | 277.5 |
| QY | 2692 | AGCTTTAAACCGGTGGACGATGGTGGTGGAGGCGATCAAGATGGGCGAGTAAAGAGAGC     | 275.1 |
| Db | 2776 | AGCTTCACACCTGTGGATGTAATGGCTGTGGATGCCATCCAGATAGCCATACAGAGAGAGC   | 283.5 |
| QY | 2752 | TTGCGCAATGCGCGCTTCACCTCTTTGACGTGTGTCTCAGATGATGAGGACATT          | 281.1 |
| Db | 2836 | TTTCCCTAGTCTGGCTTCACACCTTTGATATAGTATCAATGACTGTAGAGACATT         | 289.5 |
| QY | 2812 | CTCCGGGTTGGGGTCACTTTGGTGTGGCCACCGAAAAAATCCTAGACAGATCCAGTG       | 287.1 |
| Db | 2896 | CTACGAGTTGGGGTCACTTTAGCGAGSACACCGAAGAAAATTTCTACACGATCCAGGTG     | 295.5 |
| QY | 2872 | ATGCGGGCGAGATGAAACACAGATTCAGTGTGTGGAGTTTGAATTCACCTGCCCTGGCT     | 293.1 |
| Db | 2956 | ATGAGACACACAGATGAACCAAAATTCAGTCTGTGGAGAGTTGTATGACACACAGCTCCTGTG | 301.5 |
| QY | 2932 | CACCTTTCTCCAAAGCCCCGCCCCC                                       | 295.7 |
| Db | 3016 | CTCCACTTCTGTAGGCGCTGGCTGCC                                      | 304.1 |

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1      RESULT      6
2      US-08-162-809-11
3      ; Sequence 11, Application US/08162809
4      ; Patent No. 3457048
5      ;
6      GENERAL INFORMATION:
7      ;
8      APPLICANT: Pasquale, Elena B.
9      APPLICANT: Sajjadi, Fereydoon G.
10     TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
11     TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
12     NUMBER OF SEQUENCES: 26
13     CORRESPONDENCE ADDRESSES:
14     ADDRESSEE: CAMPBELL AND FLORES
15     STREET: 4370 La Jolla Village Drive, Suite 700
16     CITY: San Diego
17     STATE: California
18     COUNTRY: United States of America
19     ZIP: 92122
20     ;
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: PatentIn Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/08/162,809
28     ;
29     FILING DATE:
30     CLASSIFICATION: 514
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Campbell, Cathryn A.
33     REGISTRATION NUMBER: 31,815
34     REFERENCE/DOCKET NUMBER: P-LJ 9503
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (619) 535-9001
37     TELEFAX: (619) 535-8949
38     INFORMATION FOR SEQ ID NO: 11:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 4097 base pairs
41     TYPE: nucleic acid
42     STRANDEDNESS: both
43     TOPOLOGY: linear
44     FEATURE:
45     NAME/KEY: CDS
46     LOCATION: 10..3042
47     US-08-162-809-11

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|                       |       |  |        |            |        |        |    |      |
|-----------------------|-------|--|--------|------------|--------|--------|----|------|
| Query Match:          | 71.8% | Score  | 2127.6 | DB 1:      | Length | 4097   |    |      |
| Best Local Similarity | 82.7% | Pred.  | No. 0  |            |        |        |    |      |
| Matches               | 2493  | Conservative   | 0      | Mismatches | 464    | Indels | 57 | Gaps |
| QY                    | 1     | CTGCTGCCCCCTGGAGAAACGGCTAATGACTCTCCACTACAGGACTGCTGACTGGC       | 60     |            |        |        |    |      |
| Db                    | 76    | CTCTGCGCCGCCCTGGAGAGACGGCTGATGAGCTCCACAAAGGGCCACAGCGACTGGG     | 135    |            |        |        |    |      |
| QY                    | 61    | TGGAATGGTATCCCTCCATCAGAGGTGGGAAAGGTGAGTGGCTCGATGAGACATGAC      | 120    |            |        |        |    |      |
| Db                    | 136   | TGATGGTGTATCTCTCTCAGAGGTGGGAAAGGTGAGTGGCTCGATGAGACATGAC        | 195    |            |        |        |    |      |
| QY                    | 121   | ACGATCGCAGCTACCAAGGTGTGCAACGTTTGTGATCAAGCCAAACACTGTGCTACGG     | 180    |            |        |        |    |      |
| Db                    | 196   | ACCATCGCACTACCAAGGTGTGCAACGTTTGTGATCAAGCCAAACACTGTGCTCGG       | 255    |            |        |        |    |      |
| QY                    | 181   | ACCAAGTTTATCCGGCGCGGTGGGGCCCAACGCCATCCACGTGGAGATGAATTTGGGTG    | 240    |            |        |        |    |      |
| Db                    | 256   | ACCAAGTATCTCCGGCGCGGTGGGGCCCAACGCCATCCACGTGGAGATGAATTTCCGTT    | 315    |            |        |        |    |      |
| QY                    | 241   | CGTGACTGCGAGCATGCCACAGCGCTGTGGCTCTCTCAAGAGAGACCTTCACCTCTAT     | 300    |            |        |        |    |      |
| Db                    | 316   | CGGAGCTGCGAGCATGCCCAACGTCCTCGAGAGACCTTCCTAAGAGACTTTTAACCTCTAT  | 375    |            |        |        |    |      |
| QY                    | 301   | TACTATGAGGCTGACTTTGACTGGCCACCAAGACCTTCCCACTGGATGGAGATGCCA      | 360    |            |        |        |    |      |
| Db                    | 376   | TACTACCAATACACACTTTGACTGTCCACCAAGACCTTTCTTAAGTGGATGGAAACCTT    | 435    |            |        |        |    |      |
| QY                    | 361   | TGGGTGAAGGTGATACCATTTGAGCGCCAGAGACTTCTCCAGAGTGAGACTTGAGTGGC    | 420    |            |        |        |    |      |
| Db                    | 436   | TGATGATAGTAAATACATTTGCTGCCAGAGAGACTTCTGCAAGTGGACTTGATGGGG      | 495    |            |        |        |    |      |
| QY                    | 421   | CGCGTCATGAAATCAACACCGAGGTGGGAGCTTGGAGCTGTGTCCCGACGGGCTTC       | 480    |            |        |        |    |      |
| Db                    | 496   | CGGCTGATGAAATTAACACCGAGGTGGGAGCTTGGAGCTGTGTCCCAAAACGGTTTC      | 555    |            |        |        |    |      |
| QY                    | 481   | TACCTGGCTTCCAGAGCATGGCGGCTGCATGTCCCATGCGCGTGCATGCTTTCTAC       | 540    |            |        |        |    |      |
| Db                    | 556   | TACCTGGCTTCCAGAGCATGGGGGGCTGCATGTCTTGTATGCAAGTCCGATCTTTTAC     | 615    |            |        |        |    |      |
| QY                    | 541   | CGCAAGTGGCCCCGATCATCAGAAATGGCGCCATCTTCAGAGAAACCTTCCGGGGCT      | 600    |            |        |        |    |      |
| Db                    | 616   | CGCAAGTGGCCCCGATCATCAGAAACGGGGGGCTTTCAGAGAAACCTTCCGGAGCG       | 675    |            |        |        |    |      |
| QY                    | 601   | GAGAGCATACCTCGTGGGTGTGCCGGGGGCACTGGATGGCAATGGGAGAGAGTGGAT      | 660    |            |        |        |    |      |
| Db                    | 676   | GAGAGCATACCTCGTGGGTGTGCCGGGGGCACTGGATGGCAATGGGAGAGAGTGGAT      | 735    |            |        |        |    |      |
| QY                    | 661   | GTACCATCATCAAGTCTACTGTAAACGGGGAGCGCGAGTGGCTGTGGCCATCGGGCGTCC   | 720    |            |        |        |    |      |
| Db                    | 736   | GTGCGCATCATCAAGTCTACTGTAAACGGGGAGTGGGAGTGGCTGTGGCCATCGGGCGTCC  | 795    |            |        |        |    |      |
| QY                    | 721   | ATGTGTCAACAGAGCTTCCAGGCGCTTGAGAAATGGCACCGTGTGCCGAGGTTCCTCACT   | 780    |            |        |        |    |      |
| Db                    | 796   | ATGTGTCAAGGCGGAGCTATGAGTGGTGGGAAATGGGAGCCGTGTGAGAGCTGGCCATCA   | 855    |            |        |        |    |      |
| QY                    | 781   | GGGACTTTCAAGGCAACAGGGAGTGAAGGCTGTACCACTGTCCCATCAAGAGCGGG       | 840    |            |        |        |    |      |
| Db                    | 856   | GGGACTTTCAAGGCAACAGGGAGTGAAGGATGTGTCCATTTGTCCAAATTAACAGCGGG    | 915    |            |        |        |    |      |
| QY                    | 841   | ACGACTTCTGAAGGGGCCACCAACTGTGTGTGCCGATGTGCTACTACAGAGCAGACTG     | 900    |            |        |        |    |      |
| Db                    | 916   | ACGACTTCTGAAGGGGCCACCAAGAACTCGTGTGCCGAAAGGATTAATTAACGGGCAAGTCT | 975    |            |        |        |    |      |
| QY                    | 901   | GACCCCTGGAGCATCCCTCTGCACCAACCATCCCTCGCGCCCAAGGCTGTATTTCCAGT    | 960    |            |        |        |    |      |
| Db                    | 976   | GACCCCTGGAGCATCCCTCTGCACCAACCATCCCTCGCGCCCAAGGCTGTATTTCCAGC    | 1035   |            |        |        |    |      |
| QY                    | 961   | GTCATAGAGACTTCCCTCATGCTGAGTGGAGCCCTTCCCGGAGCTCGGAGGCCAGAG      | 1020   |            |        |        |    |      |
| Db                    | 1036  | GTCATAGAAACCTCCGATGCTGAGTGGAGCCCAACAGAGACTTCAAGGGGGCGGAG       | 1095   |            |        |        |    |      |
| QY                    | 1021  | GACCTGCTTACCAATCATCTGTCAAGAGCTGTGGCTGGGGCGGGGGTCTGTCAACCCG     | 1080   |            |        |        |    |      |



CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ. ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3546 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..2920  
US-08-162-809-9

Query Match 53.4%; Score 1581.6; DB 1; Length 3546;  
Best Local Similarity 73.1%; Pred. No. 0;  
Matches 2114; Conservative 0; Mismatches 734; Indels 42; Gaps 5;

43 GCACAGCTGAGTGGGGCTGAGTGGTCACTCCATCAACGAGGAGGAGGAGGCG 102  
DB 59 GTACCTCGAGGTGGAGTGGATGACACCACTCCGAGAGCGGGTGGAGAGGTAGTGT 118  
QY 103 TAGCATGAGAACATGAACAGATCCGACGTACACAGGTGTGCAACGTGTTGAGTCAAGC 162  
DB 119 TAGAGAGAGCTATGAACCCCATCCGACATACAGGTGTGCAACGTGCGGAGGCCAAC 178  
QY 163 CAGAACAACTGCTACGAGCAAGATTATCCGGCGCCGTGGGCCACCGCATCCACGTG 222  
DB 179 CAGAACAACTGCTGCGACCAAGTTCATTCAGCGCCAGGACGTCCAGCGTGTACGTG 238  
QY 223 GAGATGAAGTTTGGGCTGAGTGCAGCAGATCCCGACCGGCTGCTGCTCCGAG 282  
DB 239 GACCTGAATTACTGCGGGAGCTGCACAGACATCCCAACATCCCTGTGTTCTGCAAA 298  
QY 283 GAGACCTTCAACCTATATATGAGGCTGACTTGGACTCGGCCAACAGACCTTCC 342  
DB 299 GAACTCTCAACTCTTCTATATGAGTGCATAGCGATTCTGCTGTGCATATAGCCCT 358  
QY 343 AACTGTGAGAGATCCATGAGGTGAGGTGATACATTGACGCGCAGAGAGCTTCTC 402  
DB 359 TTCTGATGAGAAACCCCTATATCAAGTGTGATCAATTCCTCCGATGAGAGCTTCTCC 418  
QY 403 CAGGTGAGACTGGGTGGCCGCGTCATGAATAATGACACCGAGGAGGACTTCGAGCT 462  
DB 419 AAATGTGAGTCCGGCCGTG-----TGAAACACCAAGGTGGCGACACTTTGGCCG 466  
QY 463 GTGTCCCGACGCGCTTCTACTGCTGCTTCAGAGACTATGCGGAGTGCATGCTCCATC 522  
DB 467 CTGTCCAGAAATGGCTTTTATGTGGCTTTCAGAGACCTTCGAGGCGCTACGTCCCTATC 526  
QY 523 GCCGTGGGTCTTCTTACCGCAAGTGCCTCCGATCATCCAGAAATGGCGCATCTTCCAG 582  
||||| ||| ||||| || || || |||||

DB 527 TCCGTCCGGCTTCTTACAGAAATGTTCCAAACCATCGCTGGCTTGTATCTTCCG 586  
QY 583 GAAACCTGTCCGGGGCTGAGACATCGCTGTGAGTCCCGGGGACAGTGCATCGCC 642  
DB 587 GAGACCTTAACGGGGCTGAGCCACGTCCTGTATTCGCGCGGACCTGATCC 646  
QY 643 AATGGGAAGAGGTGATGATGATCAACGCTACTGTAAAGGGGAGGCGAGTGGCTG 702  
DB 647 AACGAGTGAAGTGTGTGCCCCGTGAAGCTGACTGCAACGGGTGATGGCAGTGTATG 706  
QY 703 GTGCGCATCGGGGCTGCTGATGTGCAAGCAGGCTTCAGAGCCGCTGTGAATGGCAGCTC 762  
DB 707 GTGCTGTGGAGCTGTGACGCTGTGCTGTGGTGTGACGACCATGAAGATATCCAG 766  
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QY 823 TGTCCATCAACAGCCGAGCACTTGTGAAGGGGCCACCACTGTGTGCGCATGCG 882  
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DB 887 TTCTTCGAGCAGACGCGGACCCCGCAGACAGCGCTGTGACACAGTGTGCTCAGCCCCA 946  
QY 943 CAGGCTGTGATTTCCAGTGTCAATGAGACCTCCCTCATGTGAGTGGACCCCTCCCGC 1002  
DB 947 CGCAGCTCATCTCCACAGTGAATGAGACGTCGTGGTGTGAGTGGAGAGCGCCAG 1006  
QY 1003 GACTCCGAGGCGGAGAGAGACCTGTCTACACATCATCTGCAAGAGCTGTGGCTCGGC 1062  
DB 1007 GACGCGGGCGGGGGAGTGTGACTGTCTACACGTCATGTCAAGAGTGTGAGTGGAG 1066  
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DB 1067 CGGGGTGTGAGACCTCCCTCGAGACACGTGAGTGTGCGCGCCAGCTGGGCTTC 1126  
QY 1116 -AGGCTGACCCAGCCAGCCATTTACATGATGACCTGTGCGCCACACCCAGTACACC 1173  
DB 1127 ACTGGCTCACTGATGAGCAGCATCTCATCAGAGGTGATGGCCACGCCAGTACACC 1186  
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DB 1187 TTGAGATCAGAGGCTGTGAAGGTGATGATCTCAGAGAGCCCTTACCTCCCATTTTGGC 1246  
QY 1234 TCTGTGAATCAGTACACCAACAGGAGCTTCATGCGCACTGTGCCATCATCATCAGTGC 1293  
DB 1247 TCGGTCAACATCAGACCAACAGGAGCCCATCTGCTGCCCCCATGATGATCTGCAC 1306  
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DB 1307 AGCAGCACCGGGAACAGCATGACATGTATGACTCCCGGAAAGGCCCAAGCGCATC 1366  
QY 1354 ATCTGGATATGAGTGCATGATGAGAG--GAGCTCAGTGTGATCAAGCCACA 1410  
DB 1367 ATTCTGACTATGAAATCAAGTACTCCGAGAGCAAGGCGGAGTGCAGTATGGCAAC 1426  
QY 1411 GCCATAAAGCCCCACCAACAGGCTCAG-----GGCTCAAGCGGGCGGCATGTAT 1464  
DB 1427 ACTGTCAACGACGAAGAAGTCTGGTGGCTGAGACGAGTGAAGGCAATGTCTGCTAC 1486  
QY 1465 GTCTTCAGAGTGGGAGCAGCACTGTGAGCTACGCGGCTTACAGCGGCAAGATGAC 1524  
DB 1487 ATGTGTAGAGTCCGGGCGCAGACAGTGTGATACGCGCGGATCAACCTCCCAACGAG 1546  
QY 1525 TTCCAGACATGACAGAGCCGAGTACAGACAGCATCCAGAGAAATTGCCATCATC 1584  
DB 1547 TTCCAGAGCACTCGGAGAGTGTGCTCACAGCAAGCTTTCCAGGAGCTTCCCTCATC 1606  
QY 1585 ATGGGCTCTCGGCGCTGTGCGCTGTCTCTCATTTGCTGTGATGATGCAATGCTG 1644  
DB 1607 GTGGGTTCAGCCACCGGGGAGCTGTGTGTATCTGTGTGATCTGATCTATTTGTC 1666  
||||| ||| ||||| || || || |||||





163 CAGAACAACTGGCTACGACCAAGTTATTCGCGCCGCGTGGGGCCACCCGATCCAGTG 222  
179 CAGAGCAACTGGCTTGGCACCACCAATTCATTCAGGCGCCAGGACGCTCCAGCGTGTACGTG 238  
223 GAGATGAAGTTTTCGTGGCTGATGACGACATCCCGACGCTGCTGGCTCCGTCGAG 282  
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299 GAGACCTTCAACCTCTTATCTATGAGTCAAGATACGATTTCTGCTGCAATAGGCT 358  
343 AACTGATGAGATCCATGGGTGAAGTGAAGTATACATTCAGCGGACGAGAGCTTCC 402  
359 TTCTGATGAGAGAACCCCTTATCAAGTGAATATCTGCTCGGATGAGAGCTTCTCC 418  
403 CAGGTGACCTGGGTGGCGCGCTCANGAAAATCAACACGAGGTGCGGAGCTTCGAGCT 462  
419 AACTGGAGTCCGCGCG-----TGTAACACAAAGGTGCGCAGCTTTGGGCG 466  
463 GTTCCCGGACGGCTTCTACCTGCGCTTCCAGGACTATGGCGCTGATGTCCCTATC 522  
467 CTCTCCAGAGATGGCTTTATCTGCTTCCAGGACCTGGGGGCTGCAATGCTCTATC 526  
523 GCGGTGCTGCTTCTTACCCGCAAGTCCCGCATTCAGATGCGCATCTTCAG 582  
527 TCGGTCCGGGCTTTCTACAGAAATGTTCACACACATCCCTGGCTTGTCTATCTCCG 586  
583 GAAACCTGTGGGGGCTGAGACACATGCTGGTGGCTGCGGGGACGCTGCATCGC 642  
587 GAAACCTTAAGGGGGCTGAGCCACGCTGCTGCTATTCGCGGGGACCTGCATCGC 646  
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647 AAGCGATGGAATGTCTGTCCTGAACTCTACTGCAACGCTGATGGCGAGTGGATG 706  
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1003 GACTCGGAGGCGGAGAGAGCTGCTTACCAACATCATCTGCAAGAGCTGTGGCTGGG 1062  
1007 GAGCGGGGGGGGAGATGACTGCTCTCTTATTCATACGTATCTGCAAGATGTCAGCGTGGAG 1066  
1063 CGGGGTGCTGCACCCGCTGCGGGGCAATGTACAGTACGACACGACGACGCT----- 1115  
1067 CGCGGCTGTGCGAGCGCTGCGAGCAACAGTGGAGTGTGCTGCGCGGCGAGCTGGGCTC 1126  
1116 --AGGCTTACCGAGCAGCATTTTACATCAGTACCTGTGGCCCAACACCCAGTACAC 1173  
1127 ACTGGCTTACTAGTGAAGAGCATCTACATCAGAGTGTATGGCCCAACCCCGCTACAC 1186  
1174 TTTCAGATCCAGGCTGTGAAGCGCTTACTGACACAGAGCCCTTTCGCTCGATGTCGC 1233  
1187 TTTCAGATCCAGGCGGTGAATGCAATCTCCAGCAAGAGCCCTTACCTCCCACTTTTGGC 1246

1234 TCTGTGAACATCACACCAACGACGACCTCATCGGCTGAGTGTCTATCATGATCAGGTG 1293  
1247 TCGCTCAACATCACAGACCAACGAGGAGCCCATCTGCTGCTGCTCCACCATGATCTGCAC 1306  
1294 AGCCGACCTGGACAGCATTTACCTCTGTGTGCCAGGCGGACCAACATGCGGTG 1353  
1307 AGCAGCACCGGGAACAGCATGACACTGTATGAGCTCCCGGAAAGGCCCAACGCGATC 1366  
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1367 ATTCTGACATGAAATCAAGTACTCCAGAAAGGAGCCAGGCTGAGGCTATTTGCCAAC 1426  
1411 GCCATAAAAAGCCCAACACAGGCTACG-----GGCTCAAAAGCGCGGCATCTAT 1464  
1427 ACTGTCAACGACGAGAAAGAACTGGTGGCTGAGCGGACTGAAGGCAATGCTCGTAC 1486  
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1487 ATGCTGAGGCTCGCGCGCGCACAGTGGTGAATACGCGCGCTACAGCTCCCAACGAG 1546  
1525 TTCCAGACCATGACAGAGCGGATACCAACAGCATCCAGAGGAAGTTGCCATCATC 1584  
1547 TTCCAGACGACTGCGGAGATGGCTCCACAGCAAGACTTCCAGAGGCTTCTCTCATC 1606  
1585 ATCGGCTCTCGGCGGCTGAGCTGTCTCTCATTTGCTGTGATCGCATCGT 1644  
1607 GTGGGTTCACGCAACCGGGGACATGCTGTGTGTATCTGTGTGTGATCATGCTATTTGTC 1666  
1645 TGTACAGACGCGGGGCTT-----TGAGCTGTGACTCGGAGTACAGCAAGCTGCAA 1698  
1667 TGTCTGAGAAAGGATGTTACTGAAACATCTCTGCTGCTTGGGAGGAGGAGCAG 1726  
1699 CACTACACGAGTGGCCACA-----TAACCCAGGATG 1731  
1727 CGCAACGACACAGATCCGAGTACACAGAGAGCTGCAGCAATATGCTCTGGGATG 1786  
1732 AAGATCTACATCATCTTTCACCTACGAGAGCCCAACGAGGACGAGGAGTTTGGC 1791  
1787 AAGTGTACATGATGCCCTTACCTTACCTATGAGAGCCCAATGAACTGTCCGGAAATTCGCC 1846  
1792 AAGGAATGACATCTCTGTGTCAAAATTTGACAGGCTGATCGAGAGGAGGAGTTTGGC 1851  
1847 AAGAGATGATATATCTCTGTCAAAATTTGAGAGGCTGATTTGAGAGGAGGAGTTTGGT 1906  
1852 GAGGTGACGAGTGGCCACCTGAAGCTGCCGAGCAAGAGATGATTTTGGGCAATCAAG 1911  
1907 GAGGTGCTGCTGGGCGGCTGAGAGCTGCTGGCGCGGTGATGATCTTTGTGGCAATCAAG 1966  
1912 ACCTCAAGTCCGGCTACACGAGAGACAGCGCGGACTTCTTGAAGCAAGCTCATC 1971  
1967 ACATGAAAGTGGGCTACACAGAGAGGACGCGCGGAACTTCTTGAATGAGCGACATC 2026  
1972 ATGGGCGAGTTGACCATTCACACGTCATCTCAGAGGCTGTGATGACCAAGAGCACA 2031  
2027 ATGGGCGAGTTGACCAACCCCAACATCATCTCAGAGGCGCTGTGAGCAAGAGCCCG 2086  
2032 CCTGTGATCATCTACACCGAGTTTCATGAGAAATGGCTCCCTGAGACTCTTCCGGCAA 2091  
2087 CCTGTATGATCATCTACAGAGTTTCATGAGAACTGCGGCTGTGATCTCTCCCGGCTG 2146  
2092 AAGATGGGAGTTTACAGTCACTCAGCTGAGTGGGAGTGGCTTGGGGGCAATCGAGCTGGC 2151  
2147 AATGATGGGAGTTTACGGGCTCATCGAGCTGAGGATGGGATGCTGCGAGGCAATCGCTGTCG 2206  
2152 ATGAATTACTGGCAACATGATATGTTTACACCGTGAATCTGGCTCCCGCAACATCTCTC 2211  
2207 ATGAATTACTCTCAAGAGTAACTATGTCACAGCAGAGACTGTGCTCCGCAACATCTCTG 2266  
2212 GTCAACAGCAACCTGTGTGCAAGGAGTGTGAGTGTGGGCTGTCAAGCTTTCAGAGGAG 2271  
2267 GTTAAACAGCACTGTGTGTGCAAGAGTGTGACTTGGGCTGTCCCGGCTTTTGGAGGAT 2326  
2272 GATACCTCAGACCCCACTTACACACAGTGGCTGGGCGGAAAGTTTCCCATTCGCTGGACA 2331



[illegible]

|    |                                |  |
|----|--------------------------------|--|
| ?  | APPLICATION NUMBER:            | JP 315806/1993   |
| ?  | FILING DATE:                   | 24-NOV-1993  |
| ?  | TELECOMMUNICATION INFORMATION: |  |
| ?  | TELEPHONE:                     | (202)293-7060  |
| ?  | TELEFAX:                       | (202)293-7860  |
| ?  | TELEX:                         | 6491103  |
| ?  | INFORMATION FOR SEQ ID NO: 3:  |  |
| ?  | SEQUENCE CHARACTERISTICS:      |  |
| ?  | LENGTH:                        | 4027 base pairs  |
| ?  | TYPE:                          | nucleic acid   |
| ?  | STRANDEDNESS:                  | single   |
| ?  | TOPOLOGY:                      | linear   |
| ?  | MOLECULE TYPE:                 | cdna to mRNA   |
| ?  | ORIGINAL SOURCE:               |  |
| ?  | ORGANISM:                      | rat  |
| ?  | TISSUE TYPE:                   | skeletal muscle myoblast   |
| ?  | CELL LINE:                     | L6   |
| ?  | US-08-348-143-3                |  |
| ?  | Query Match                    | 51.5%; Score 1526.4; DB 1; Length 4027;                          |
| ?  | Best Local Similarity          | 71.4%; Pred. No. 0;  |
| ?  | Matches 2083; Conservative     | 0; Mismatches 791; Indels 42; Gaps 4;                            |
| Oy | 52                             | GAGCTGGGCTGGATGTCATCTCTCATCCAGGGTGGGAAAGGTAGTGGCTACATGAG 111     |
| Db | 388                            | GAGCTGGGATGAGCATCTCATCTCAGAGAGTGGTGGGAAAGGTAGGCGCTACATGAA 447    |
| Oy | 112                            | AACATGACACAGATCCGACGATCAGGATGTCAGACGTGTGAGTTCAGACGAGAAAC 171     |
| Db | 448                            | GCCATGATTCCTATCCGACCGATACGGTGTGTAACTGCGGATCCAGCCAGAAAC 507       |
| Oy | 172                            | TGGCTACGACCACTTATTCGCGCGCGGTGGGGCCACCGCATCCAGCTGAGATGAAG 231     |
| Db | 508                            | TGGCTGCGCGACCGGTTTCATCTGCGCGGGGAAATGTCACGCGGTCTAGCTGGAGTGAAG 567 |
| Oy | 232                            | TTTTGGGCGCGATCGACGACATCCCGACGTCGCGGTCTCTGCAAGGAGACCTTC 291       |
| Db | 568                            | TTTTACCGTAGAGATTGCAACAGCATCCCGACATCTCCTGCTCTGCAAGGAAACCTTC 627   |
| Oy | 292                            | AACCTCTATTACTATGAGCGCTGACTTTGACTCGCGCACCAAGACCTTCGCCAATGATG 351  |
| Db | 628                            | AACCTTTTTTTACTAGAGGCTGATAGCGATGCGGTCAGCTCTCTCTCTCTTGATG 687      |
| Oy | 352                            | GAGATTCATGGGTGAAGTGGATACCATGTCAGCGGACGAGAGAGCTTCTCCAGGTGAC 411   |
| Db | 688                            | GAGAACCCCTTAGTGAAGATGGACACCATTTGGCCAGATGAAAGGCTTCTCGGGCTAGAC 747 |
| Oy | 412                            | CTGGGTGGCGCGGTGATGAAATCAACACCGGATGGCGAGCTTGGAGACTGTGCCGC 471     |
| Db | 748                            | GCTGGGCGC-----GTAAACACAAAGTGCAGCTTGGGGCGCTTTCGCAA 795            |
| Oy | 472                            | AGCGGCTTCTACGTGGCCTTCCAGGACTATGAGCGGCTGCATGTCCCTCATGCGCGT 531    |
| Db | 796                            | GCGGCTTCTACTGCTTGGCCTTCCAGGACCAAGGCTGCTGCATGTCACTCATCTGTGCGC 855 |
| Oy | 532                            | GTCCTTACCGCAATGGCCCCCGGACATCCAGATGGCGGCATCTTCCAGGAAACCCG 591     |
| Db | 856                            | GCTTCTTCAACAAATGTGCATCCACACTGCGAGGCTTGCACCTCTTCCGAGAACCTTC 915   |
| Oy | 592                            | TGCGGGGCTGAGAGACATCGCTGGTGGCTGCCCGGGGAGCTGCATGCCAATGGGAA 651     |
| Db | 916                            | ACGGGGGCTGAGGCCACATTCGCTGGTCAATGGCCCTGGGACCTGCATGCTTAACGCTG 975  |
| Oy | 652                            | GAGTGTGATGTACCATCAAGCTTACTGTAAACGGGAGCGGAGTGGTGGTCCCATC 711      |
| Db | 976                            | GAGGTGTCTGTACCCCTCAAGCTTACTGTCAATGGCGAGGGGAGTGGATGTGCCCGTT 1035  |
| Oy | 712                            | GGGCGCTCATGTGAAAGACAGCTTTCGAGCGGCTTGAAGATGAGCACTCTGCGGAGGT 771   |
| Db | 1036                           | GGTGCTGCACTGCGGCTACTGCGCATGAGCCAGCCGCGCAAGAGACCAAGTGGCGGCGC 1095 |
| Oy | 772                            | TGTTCATCTGGGACTTTTCAAGGCAACCAAGGGATGAGGCGCTGTACCATCTGTCCATC 831  |





1357 CTGGACTATGAGTGCAGTACTATGAGAAAGAGCTGATGATGACACCCACAGCCATA 1416  
1696 TTGGACTATGAGTGCAGTACTATGAGAAAGAGCTGATGATGACACCCACAGCCATA 1755  
1417 AAAAGCCCAACCAACAGGCGACGAGCGCCCAAAAGCGCGCCATCATGCTTCCAGGTG 1476  
1756 CAGAGACTCTGTACACTGAGAGGACGACGAGCGCCGAGCGCCGATATGATGATGATG 1815  
1477 CGGAGCAGACTGTGAGAGCTACGAGCGCGCTACAGCGCGCAAGATGATGATGATGATG 1536  
1816 CGGAGCTGAGAGTACAGAGTATGAGAGGATGATGAGCGCGCCAGCTGATGATGATGATG 1875  
1537 ACAGAGCCGAGTACAGAGC---AAGCTACAGAGAGAGTGTGCTGATGATGATGATG 1593  
1876 AGTGAAGAGGCTGAGAGGCGCGAGAGCTGATGATGATGATGATGATGATGATGATG 1935  
1594 TCGGCGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1653  
1936 ACCTGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1995  
1654 CGGAGCTGTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713  
1996 AAGCAGGCGAGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2044  
1714 CACATACCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773  
2045 -ACGTTGCGCGCGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2103  
1774 GCAGTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 1833  
2104 GCGCTGCGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2163  
1834 GAGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1893  
2164 GAGAGTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2223  
1894 ATCTTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 1953  
2224 GTGTGCTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2283  
1954 CTGAGCAGAGCTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2013  
2284 CTGAGTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2343  
2014 GTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2073  
2344 GTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2403  
2074 GACTGCTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2133  
2404 GACTGCTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2463  
2134 CGGAGCAGAGCTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2193  
2464 CGTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2253  
2194 GCTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2253  
2524 GCTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2583  
2524 TCAAGCTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2313  
2584 TCCGCTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2643  
2314 TTCCCATTCGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2373  
2644 ATCCCTATTCGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2703  
2374 GATGTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2433  
2704 GATGTGTGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2763

2434 TGGAGATGAGACCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2493  
2764 TGGAGATGAGACCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2823  
2494 CCATGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2553  
2824 CCATGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2883  
2554 AACCCAGGCGCGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2613  
2884 AACCTGAGGCGCGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2943  
2614 AACAGCTTCAAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2673  
2944 GCGAGCTTCAAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 3003  
2674 ACAGTCCCGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2733  
3004 ACAGTCCCGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 3063  
2734 GGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 2793  
3064 GGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 3123  
2794 ATGATGATGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 2853  
3124 ATGATGATGAGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATG 3183  
2854 CTGACAGTGTGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 2913  
3184 CTGACAGTGTGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 3243  
2914 CATTCAGTGTGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 2949  
3244 CGCTCAGTGTGAGAGGAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 3279

RESULT 11  
US-08-571-785-3  
; Sequence 3, Application US/08571785  
; Patent No. 5804411  
; GENERAL INFORMATION:  
; APPLICANT: TAJIMA, HISAO  
; APPLICANT: KITAGAWA, KOICHIRO  
; APPLICANT: OHNO, HIROYUKI  
; APPLICANT: OHNO, TOSHIO  
; TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140  
; TITLE OF INVENTION: and DNAS encoding it  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; City: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/571,785  
; FILING DATE: 13-DEC-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/348,143  
; FILING DATE: 23-NOV-1994  
; APPLICATION NUMBER: JP 315806/1993  
; FILING DATE: 24-NOV-1993  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860

TELEX: 6491103  
: INFORMATION FOR SEQ ID NO: 3:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 4027 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA to mRNA  
: ORIGINAL SOURCE:  
: ORGANISM: rat  
: TISSUE TYPE: skeletal muscle myoblast  
: CELL LINE: L6  
: US-08-571-785-3

Query Match 51.5%; Score 1526.4; DB 1; Length 4027;  
Best Local Similarity 71.4%; Pred. No. 0;

Matches 2083; Conservative 0; Mismatches 791; Indels 42; Gaps 4;

OY 52 GAGCTGGCGTGGATGGTGCATCTCCATCAAGGTGGAGAGGTAGTGGCTACGATGAG 111  
Db 388 GAGCTGGCGTGGATGGTGCATCTCCATCAAGGTGGAGAGGTAGTGGCTACGATGAA 447  
OY 112 AACATGAAACGATCCGCAAGTACAGGTGTGCAAGGTGTTGAGTCAAGCCAGAACAC 171  
Db 448 GCCATGATCTTCCGCAAGTATCAGGTGTGAGTGTGACGTGCGGAGTCCAGCCAGAACAC 507  
OY 172 TGCGTACGACCAAGTTTATCCGCGCGCTGGGGCCACCGCATCCAGCTGAGATGAAG 231  
Db 508 TGCGTACGACCAAGTTTATCCGCGCGCTGGGGCCACCGCATCCAGCTGAGATGAAG 567  
OY 232 TTTTCGCGTGTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 291  
Db 568 TTTACGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627  
OY 292 AACCTTATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 351  
Db 628 AACCTTATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 687  
OY 352 GAGAAATCCATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411  
Db 688 GAGAAATCCATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 747  
OY 412 CTGGGTGGCGCGGTATGAAATCAACACGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 471  
Db 748 GCTGGGCGC-----GTTAAACAACAAAGTGGCGAGTGGCGCGCTTTTCACAA 795  
OY 472 ACGGCTTCTACCTGCGCTTCCAGAGATGATGAGGCTGATGCTGATGCTGATGCTGCTG 531  
Db 796 GCGGCTTCTACCTGCGCTTCCAGAGATGATGAGGCTGATGCTGATGCTGATGCTGCTG 855  
OY 532 GTCTTCTACCGCAAGTGGCGCGCGCATCCAGATGAGGATGAGGATGAGGATGAGGATGAG 591  
Db 856 GCGTCTTCTACCGCAAGTGGCGCGCATCCAGAGTGGCGCGCATCCAGAGTGGCGCGCAT 915  
OY 592 TCGGGGCTGAGAGACATCGCTGGTGGCTGCCGGGCGAGCTGATGCTGATGCTGATGCTG 651  
Db 916 ACGGGGCTGAGAGACATCGCTGGTGGCTGCCGGGCGAGCTGATGCTGATGCTGATGCTG 975  
OY 652 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711  
Db 976 GAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1035  
OY 712 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771  
Db 1036 GGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1095  
OY 772 TGTCCATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 831  
Db 1096 TGTCCATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1155  
OY 832 AACAGCCGAGACACTTGTGAAGGGGCGACCAACTGTGTCTGCGCAATGCTCTACTACAGA 891  
Db 1155 TGTCCATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1215

Db 1156 AATAGCCGACACCACTCGCCGCGCTGCGACATCTGACACTGTACAAATATTCTACCGC 1215  
OY 892 GCAGACCTGACCCCTGGACATGCCCTGACACACCATCCCTCGCGCCGACGAGCTGTG 951  
Db 1216 GCAGACCTGACACAGCGGACGCGCTGACACAGCGGTGCGCTGCTCCCGCGGAGTGTG 1275  
OY 952 ATTTCAGTGTGAATGAGACCTCCCTCATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1011  
Db 1276 ATTTCAGTGTGAATGAGACCTCCCTCATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1335  
OY 1012 GCGCGAGAGAGACCTGCTGATCAACATCTGACAGAGCT-----GTGGC 1036  
Db 1336 GCGCGAGAGAGACCTGCTGATCAACATCTGACAGAGCT-----GTGGC 1395  
OY 1036 GCGCGAGAGAGACCTGCTGATCAACATCTGACAGAGCT-----GTGGC 1095  
Db 1396 GCGCGAGAGAGACCTGCTGATCAACATCTGACAGAGCT-----GTGGC 1455  
OY 1117 GCGCTGACCGGACCGGATTTACATGATGATGATGATGATGATGATGATGATGATGATG 1176  
Db 1456 GCGCTGACCGGACCGGATTTACATGATGATGATGATGATGATGATGATGATGATGATG 1515  
OY 1177 GAGATCCAGGCTGTGAAAGGCGTTACTGACAGAGCCCTTCTGCGCTGATGCTGCTG 1236  
Db 1516 GAGATCCAGGCTGTGAAAGGCGTTACTGACAGAGCCCTTCTGCGCTGATGCTGCTG 1575  
OY 1237 GTGAATCATCACCACCAACCAAGGAGCTTCATGCGAGTGTGATGATGATGATGATGATG 1396  
Db 1576 GTGAATCATCACCACCAACCAAGGAGCTTCATGCGAGTGTGATGATGATGATGATGATG 1635  
OY 1297 GCGACCGTGTGACAGCATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1356  
Db 1636 AGTTCAAGGAGACACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1695  
OY 1357 CTGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1416  
Db 1696 CTGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1755  
OY 1417 AAAAGCCCGACCAACGAGTACAGGCGCTCAAAAGCGGCGCGCTGATGCTGCTGCTGCTG 1476  
Db 1756 CAGAAAGAACTGTGACAACTGAGAGGAGTGCAGGCGCGCGCTGATGCTGCTGCTGCTG 1815  
OY 1477 CCGGACACGACTGTGAGGAGCTACAGGCGCTGACAGGCGCGCTGATGCTGCTGCTGCTG 1536  
Db 1816 CCGGACACGACTGTGAGGAGCTACAGGCGCTGACAGGCGCGCTGATGCTGCTGCTGCTG 1875  
OY 1537 ACAGAAACCGAGTACAGGAGC---AAGCATCCAGAGAAAGTGGCACTGATGCTGCTGCTG 1593  
Db 1876 ACAGAAACCGAGTACAGGAGC---AAGCATCCAGAGAAAGTGGCACTGATGCTGCTGCTG 1935  
OY 1594 TCGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1653  
Db 1936 TCGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1995  
OY 1654 CCGGGGCTTGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713  
Db 1996 CCGGGGCTTGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2044  
OY 1714 CACATACCCCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1773  
Db 2045 -ACGTGCGCGCGCGAGATGAAAGTTTACATTTGACCTTACTGACGAGATGCTCAATGAG 2103  
OY 1774 GCACTGCGGAGGATGTTGCCAAGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1833  
Db 2104 GCACTGCGGAGGATGTTGCCAAGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2163  
OY 1834 CGAGCAGGAGGATGTTGCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1893  
Db 2164 CGAGCAGGAGGATGTTGCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2233  
OY 1894 ATCTTTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1953  
Db 2234 ATCTTTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2283

RESULT 12  
US-08-571-785-4  
; Sequence 4, Application US/08571785

| Query Match           | 51.5%;       | Score 1526.4;   | DB 1;           | Length 4027; |
|-----------------------|--------------|---|-----------------|--------------|
| Best Local Similarity | 71.4%;       | Pred. No. 0;  |                 |              |
| Matches 2083;         | Conservative | 0;  | Mismatches 791; | Indels 42;   |
|                       |              |   |                 | Gaps 4;      |
| QY                    | 52           | GAGCTGGGCTGATGCTGGCATCCTCCATCAGGGGTGGGAAGAGTGAATGGCTACAGATGAG | 111             |              |
|                       |              |   |                 |              |
| Db                    | 388          | GAGCTGCGATGACATCTCATCCAGAGAGTGGGTGGGAAGAGACGGCTACGATGAGAA     | 447             |              |
| QY                    | 112          | AACATGAACAGATCCGCGACATGACAGATGTGTCAACAGTGTGATCAAGCCAGAACAC    | 171             |              |
|                       |              |   |                 |              |
| Db                    | 448          | GCCATGATCTCTATCCGACAGTATCAGGTGTATACGTGCGCGATCCAGCCAAACAC      | 507             |              |
| QY                    | 172          | TGGCTACGACCAAGTTTATCCGGGCGCGTGGGGGCCCAACCCGATCCAGAGTATCAAG    | 231             |              |
|                       |              |   |                 |              |
| Db                    | 508          | TGGTGGCGGACCGTTTCACTGGGGCGCGGAATGCCAGCGGGTCTACGTGAGACTAAG     | 567             |              |
| QY                    | 232          | TTTTCCGCTGGGTACATGCAGACAGATCCCGACAGCTGTGGCTCTCGCAAGAGACCTTC   | 291             |              |
|                       |              |   |                 |              |
| Db                    | 568          | TTTACCGTGAAGATTTGCACAGACATCCCAACATCTCCTGGCTCTCGCAAGAACCTTC    | 627             |              |
| QY                    | 292          | AACCTATTACTATATGAGGCTGACTTTGACTGGGGCCACCAAGACCTTCCCAACTGTGATG | 351             |              |



Db 628 AACCTTTTACTAGAGGCTGTATAGCATGTGGCTGAGCCCTCTCTCCCTTCTGGAG 687  
OY 352 GAGATTCATGGGTAGAGGTGATACATTTGAGCCGACAGAGGCTTCTCCAGGTGAC 411  
Db 688 GAGAACCCCTAGTAAAGTGTGACACACATTTGGCCAGATGAGAGCTTCTCGGGCTAGAC 747  
OY 412 CTGGGTGGCCGCGTCATGAAATCAACACCGAGGTGGAGAGCTTGGAGCTGTGTCCGC 471  
Db 748 GCTGGGCGC-----GTTAAACACCAAAAGTGGCAGCTTGGGCGCTTCCAA 795  
OY 472 AGCGGCTTACCTGACCTTCCAGCATATGGCGGCTGATCTCCCTCAATGCCCTGCGT 531  
Db 796 GCGGCTTCTACTGTGGCTTCCAGACCAAGGCTGCTGATGTCACTCTCTGTGTGCGC 855  
OY 532 GTCTTCTACCCGAGTGGCCCCCGCATTCATCCAGAAATGGCGCATTTCTCAGSAAACCTG 591  
Db 856 GCGTCTCTAAGAAAGTGTGATCCACACATGACAGGCTTGGCACTCTTCCCGCAGACCTTC 915  
OY 592 TCGGGGCTGAGAGCATCGCTGTGGCTGCGCGGCGAGCTGCATGCCAATGCCGAA 651  
Db 916 ACGGGGCTGAGCCCATCTTCCGTGTGATTTGCCCTGGACCTGATCGTAACGCTGTG 975  
OY 652 GAGGTGATGTATCCCATCAAGCTCTACTGTACAGGGGACGGGAGTGGGTGGTCCCATC 711  
Db 976 GAGGTGTGTGACCGCTCAAGCTCTACTGTGCAATGGCGAGAGGGAGTGGATGGTCCGTT 1035  
OY 712 GGGGCTCATGTGCAAAAGCATGCTTCCAGGCGCTTGAGAAATGGGACCCCTGCGSAGGT 771  
Db 1036 GGTGCTGTCACTGCGCTACTGTGCTATGACCAAGCCCGCAGAGAACCCAGTGGCGCGC 1095  
OY 772 TGTTCATGTGGACTTTTCAAGGCAACCAAGGGATGAGGCGCTGTACCCACTGTCCATC 831  
Db 1096 TGTCCCTCCGAGGATGACAAAGCAAGGAGAGGGGCGCTGCTCCCTCCCTCCCGCC 1155  
OY 832 AACACCCGAGCACTTCTGAAAGGGCCACCAACTGTGTCTGCGCGAATGGCTACTACAGA 891  
Db 1156 AATACCCGACCACTGCGCGGCTGACACATCTGACCTGTGCAAAATTAATTTTACCCG 1215  
OY 892 GCAGACTGAGACCCCTGGACATATGCTGACACACATCCCTTCCGCGCCAGAGCTGTG 951  
Db 1216 GCAGACTGACAGACAGCGGACAGCGCTGACACAGGTGCTGCTTCCCGCGGGGTGTG 1275  
OY 952 AATTCAGTGTCAATGAGACCTCTCTCATGTGTGAGTGGACCCCTCCCGGACTCCGGA 1011  
Db 1276 AATCTCAATGTAAATGAGACCTCGCTGATCTCGATGTGAGTGGACCCCGGAGCTTGGC 1335  
OY 1012 GGCAGAGAGACCTGCTCTACAAACATCATCTGCAAGCT-----CTGCG 1056  
Db 1336 GAGAGAGATGACCTCTCTTATATATGTATCTGTAAAGATGCCGTGGAGCTCTGGGCT 1395  
OY 1057 TCGGGCCGGGTGCTGACCCGCTGCGGGGACAAATGTACAGTACGACACGCGACTA 1116  
Db 1396 GAGAGTCCGGGACCTGTTACAGCTGTGATGACAAAGTGTGAGTTCAGAGCCGACAGCTG 1455  
OY 1117 GGCCTGACCGACCAAGCATTTATCATAGTGAACCTGTGGCCACACCCAGTACACCTTC 1176  
Db 1456 GGCCTGACCGACGAGCGCGGTCCACATCAGCCACTGTTGGCCACACCGGCTACACCTTT 1515  
OY 1177 GAGATTCAGAGCTGTGAAGCGGCTTACTGACAGAGCCCTTCTCGGCTAGTTCGCTCT 1236  
Db 1516 GAGGTGACAGGCTGTCAACGCGCTCTGTGGCAAAAGCCCTTTCGCGCCGCTATGAGGT 1575  
OY 1237 GTGAAATCACCACCAAGGAGGAGCTGACGCGAGTGTCCATCTGATCAGTGTGAGC 1296  
Db 1576 GTGAAATATACCAACCAAGGAGCGCCCATCAGAAAGTGTCTTCCACTTTCAGACAC 1635  
OY 1297 GCGACCGTGGAGCATTAACCTGTGTGTGTCCACCGGAGCAGCCCAATGGCGTATC 1356  
Db 1636 AATTGAGGAGAGCGCTGACCTGTCTGTGGACCCCGGAGCGGCTTAACGAGTATC 1695  
OY 1357 CTGGAGTATGAGACTGTACATGTAGAAAGAGTCAAGTGTGATCAACGCCACAGCCATA 1416  
||||| ||||| ||||| || ||| ||| ||| |||||

Db 1696 TTGACATATGAGATGAAGTACTTTTGAAGAAGTAAAGGATCGCTCCACTGTCAACAC 1755  
OY 1417 AAAAGCCCCACCAACAGGTCAGCGGCTCAAAAGCCGCGCCATCATGTCTTCCAGGTG 1476  
Db 1756 CAGAAAGCTGTGTCAACTGTGACGAGTGTGACGCCGACGCCCGGTATGTATTCAGGTC 1815  
OY 1477 CGGGACGCACTGTGGCAGGCTTACGGGGCTTACAGCGGCAAGATGTACTTCCAGACATG 1536  
Db 1816 CGGGCTGCAAGTGTAGAGTGTACGAGCTGTATACCGCGCAGCTGAGTTTGTAGACACAG 1875  
OY 1537 ACAGAGCCGATACCAGAC---AAGCATCCAGGAAAGTTGCACTCATCGAGCTTC 1593  
Db 1876 AGTGAAGAGGCTCAGGGGCCAGGACGCTTCAAGAGCAGCTTCCCTTAATTTGGGATCC 1935  
OY 1594 TCGGCGCTGTGGCTGTCTTCCATTTGCTGTGTGTTCATGCGCATCGTGTAAACAGA 1653  
Db 1936 ACCGTAGCGGCTTGTGTATGTGGTGGTGTGCTGTGTATGTGTCTGTGTGCGTCAAG 1995  
OY 1654 CGGGGTTTGAAGCTGTGTGCTGTGAGTGTACAGGATACAGGACAGCTCAACACTACAC 1713  
Db 1996 AAGCAGCGCGCAGGCGCTGATGACAGAAATACAGGAGAAAGTTGCACCAAT----- 2044  
OY 1714 CACATACCCCGAGGATGAAGATCTACATCGATCTTTCACCTAGGAGACCCCAACGAG 1773  
Db 2045 -ACGTTGCCCCAGATGAAGTTTACATTTGACCCCTTACTACGAGAGATCCAAATGAG 2103  
OY 1774 GCAGTGCAGGAGTTTGCACAGAAATTTGACATCTCTGTGTCAAAATTTGAGCAGGTGATC 1833  
Db 2104 GCGGTCCGAGATTTGCGCAAGGATGATGTGTCTGTGCTCAAGATGAGAGGTGAT 2163  
OY 1834 GGAGCAGGGGATTTGGCAGGTCTGTGAGTGGCCACTGTGAAGCTCCAGCAGAGAGAG 1893  
Db 2164 GGAGCTGGGAGATTTGGGAAAGTGTGCGGGGTGCGGTGAACCTGCCGCGCGGAG 2223  
OY 1894 ATCTTGTGGCCATCAAGAGCTGTCAAGTGTGGGCTACAGGAGAAAGAGCGCGGAGCTTC 1953  
Db 2224 GTTGTGTGGCCATCAAGCACTGTGAAGTGTGATACAGGAGGAGGAGGCGGAGCTTC 2283  
OY 1954 CTGACGGAAGCTCCATCATATGGGCGCAGTTGACATCCCAAGCTGATCCACTGAGAGGT 2013  
Db 2284 CTGAGTGAAGGCTTCATCATATGGGTCAATTTGACCAATCCAAATATATATGCTGTAGAGG 2343  
OY 2014 GTCTGACCAAGACACACCTGTGATGATCATCAGGAGTTATGAGAAATGCTCCCTG 2073  
Db 2344 GTGTGACCAAAAGTGTGCTCACTGTGATGTCTGATGATGTATGAGAACTGTGCCCTG 2403  
OY 2074 GACTCTTCTTCCGCAAAAGATGGAGTGTACAGTGTATGATGATGATGATGATGATGAT 2133  
Db 2404 GACTCTTCTTACGGCTCATATGACGGGCTTACAGTGTATGATGATGATGATGATGATG 2463  
OY 2134 CGGGCATGCGAGCTGTGCAATGAAGTACCTGTGAGACATGAACTATGTTCACCGTGA 2193  
Db 2464 CGTGGCATGTGTGCGGCGAGTAAGTACTGTGTGATGATGATGATGATGATGATGATG 2523  
OY 2194 GCTGCGCGCAACATCTGCTCAACAGCAACCTGTGTGCAAGTGTGCAAGTGTGCAAGTGT 2253  
Db 2524 GCTGCGCGCAACATCTTGTCAACAGTAACCTGTGTGCAAGTGTGCAAGTGTGCAAGTGT 2583  
OY 2254 TCAGGCTTCTAGAGAGATCTGACAGCCACCTACAGCAGTGTGAGTGTGAGTGTGAGTGT 2313  
Db 2584 TCCCGCTTCTGAGAGACACCCCTGACAGCCACCTTACACAGCTCTCTGGGTGGAGAG 2643  
OY 2314 TTCCCATTCGCTGTGACAGCCCGGAGGACATCAAGTGTACCGGAAGTTCACCTGCGCA 2373  
Db 2644 ATTCCTATTCGTTGGACCGCCAGAGGCGCATATGAGTATCGGAAGTTCAGCTGTGCA 2703  
OY 2374 GATGTGTGAGCTTAGGCAATTTGATGTGTGAGTGTATGCTATGTGTGAGGAGGCGCTTAC 2433  
Db 2704 GATGTGTGAGCTTAGGCAATTTGATGTGTGAGTGTATGCTATGTGTGAGGAGGCGCTTAC 2493  
OY 2434 TGGGACATGACCAAGAGATGTAATCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2493  
Db 2764 TGGGACATGACCAAGAGATGTAATCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2823  
||||| ||||| ||||| || ||| ||| ||| |||||



|    |      |  |     |
|----|------|--|-----|
| OY | 2494 | CCCATGGACCTCCCGAGCGCCGCGACCAACATCATCTGTGACATGTTGGCGAAGGACCGC     | 255 |
| Db | 2824 | CCCATGGACCTCCCGAGCGCGCGCTGCACCACTATCTGTGACTGTTGGGTGGGGAACGG      | 288 |
| OY | 2554 | AACCAACGGGCCCAAGTTCGGCGCAATTTGTGCACACGCTAGACAAAGATGATTCGCAATCC   | 261 |
| Db | 2884 | AACCTCAGGCCCAAGTTCCTCCCAATGTGCACACGCTAGACAAAGTATTCGCAATGCT       | 294 |
| OY | 2614 | AACAGCTCMAAGCCATGCGGGCCCCCTCTCTCTGTGCATCAACCTGCGCTGCTGCACGC      | 267 |
| Db | 2944 | GCCAGCCCTCAAGGTCATCGCCAGTGGCCCCATCTGGGCGATGTCCAGGCCCTCTCTAACACGC | 300 |
| OY | 2674 | ACGATCCCCGCATCTACACACACTTTTAACACGATGAGAGAGGCGTGGAGGCCATCAAGATG   | 273 |
| Db | 3004 | ACGGTCCCAAGTTTATACGACCTTCACGACGCGTGGGCGACTGGCTATAGATCCATCAAGATG  | 306 |
| OY | 2734 | GGGCAGTACAAAGAGAGCTTGGCCAAATCCCGGCTTCACCTCTTGAACGTCGTGCTAG       | 279 |
| Db | 3064 | GGGAGGATTAAGAGACCTTCGTGCGGGGCTTTGCTCCTTGTACCTGGTGGCCAG           | 312 |
| OY | 2794 | ATGATGATGGAAGGACATCTCCCGGCTTGGGGTCACCTTGGCTGGCCACCAAGAAAAATC     | 285 |
| Db | 3124 | ATGACTGCAGAGATCTGCTTAAGGATGTGGGGTCACTTGGCCGCGCACCAAGAAAGATC      | 318 |
| OY | 2854 | CTGAACAGTATCCAGGTGATGCGGCGCGAGATGAACCAATTCAGCTGTGGAGTTTTGA       | 291 |
| Db | 3184 | CTCAGCAGTATTCAGGACATGCGGCTGCGAGATGAACCAAGACACTGCCGTGCAGGTTCTGA   | 324 |
| OY | 2914 | CATTCACTGCTGCTGGCTCAACCTCTTCCTCAAGCC                             | 294 |
| Db | 3244 | CGCTCAGCTCAGGAGGCGCGTGGGCCCCCGGAGC                               | 327 |

|    |      |  |      |
|----|------|--|------|
| Oy | 952  | ATTTCACGTGCAATGTGACCTCCCTCCATGCGTGGAGTGGAGACCCCTCCCGGCACTCCGGA   | 1011 |
| Db | 1015 | ATCTCCATGTGTAATGTGACCTCGCTGTATCTCTGATGGATGGAGTGAACCCCGGACTTGTGC  | 1074 |
| Oy | 1012 | GGCCGAGAGGACCTCGCTCAACATCATCTGCAAGAGCT-----GTGGC                 | 1056 |
| Db | 1075 | GGACGAGATGACCTCTTATTAATGTATTCTGTAAAGATGGCGGTGGAGCTCTGGGCT        | 1134 |
| Oy | 1057 | TCGGGCGGGGTGCTCTACACCCGCTGGGGACAAATGTACAAGTACGACACACCGCAGCTA     | 1116 |
| Db | 1135 | GGAGGTCCGGGACCTCTTACAGCTGTGATGACAAACGTGAGATTGGAGCCCGACAGCTG      | 1194 |
| Oy | 1117 | GGCCGTGACCGGACCATTTATCAATCAGTGAACCTCTGGCCACACCGACAGTACACCTTC     | 1176 |
| Db | 1195 | GGCCTTGACCGAGCGCCGGGTCCATATAGCACACTTCTTGCCACACACCGCTACACCTTT     | 1254 |
| Oy | 1177 | GAGATCCAGGCTGTGAACGGCGTTTACTGACACAGAGCCCTTCCTGCGCTCAGTTCCGCTCT   | 1238 |
| Db | 1255 | GAGGTGACGGCTGTCAACGGCGCTCTCTGGGAAAGGCCCTTTGCGCGCCCGCTATGACACT    | 1314 |
| Oy | 1237 | GTGAACATCACACACCAACGAGCACTCCATCGGCAAGTGTCCATCATCATGATAGGTGAGC    | 1296 |
| Db | 1315 | GTGAATATCACACCAACCAAGGCGCCCATCAAGAAAGTCTCAACCTCCACTTGCACAGC      | 1374 |
| Oy | 1297 | CGCACCGGACACATTTACCCTCTGCTGGTGTCCACCGGACACGACCAATGAGCGTGAATC     | 1356 |
| Db | 1375 | AGTTTCAGGAGACACCTGACACCTGTCTGTGGGACACCCCGGAGCGGCTTACGGAATCATC    | 1434 |
| Oy | 1357 | CTGGAATAGAGTCACTATGAAAGAGCACTCAGTAGATACAAACGCAACGCATATA          | 1416 |
| Db | 1435 | TTGGACATATGATGATGAGTACTTTGAAAGAGTAAAGGCATGGCTCCACCTGTACACAGC     | 1494 |
| Oy | 1417 | AAAAGCCCCAACACAGGTACAGGGGCTTCAAGCCGGGGCCATCTATGTCTTCCAGGTG       | 1478 |
| Db | 1495 | CAGAAGAACTCTGTACAACTGAGCAGGACGTGCACACCCGACCGCGCTATGTAACTTGAAGTTC | 1554 |
| Oy | 1477 | CGGCGACGCACTGTGGGAGGCTTACGGGCGCTACAGCGCAAGATGACTTCCAGACATGT      | 1538 |
| Db | 1555 | CGGGCTGCAACAGTACGAGGTTTACGGACAAATATAGCCGCCACAGCTGAGTTTAAACACAG   | 1614 |
| Oy | 1537 | ACAGAAAGCCAGTACACGAGC---AAGCATTCAGAGAAAGTTGCCACTCATCTGCGGCTCC    | 1593 |
| Db | 1615 | AGTGAAGAGAGCTCAGGGGCGCCACAGAGCTTCAAGACACACTTCCCTTAATTGTGGAGTCC   | 1674 |
| Oy | 1594 | TCGGCCGCTGGCCCTGGCTTCTTCATTTGCTGTGTGTCATGTGCCATGTGTGTAAACGA      | 1655 |
| Db | 1675 | ACCGTACTGTGCTTTGTCTTCAATGATGGTGTGTGTGTGATTTGTCTTGTCTCCACAG       | 1734 |
| Oy | 1654 | CGGGGGTTTGAAGCTGTGTGACTCGAGATACAGGCAACACTCAACACTACACAGTGGC       | 1713 |
| Db | 1735 | AAGCAGCGCCAGGGGCTGTATGCAAGATACACGAGAAATTTGCACAAT-----            | 1788 |
| Oy | 1714 | CACATTAACCCGAGCATGAAGATCTACATCGATCTTTCACTACGAGAGACCCCAACAG       | 1773 |
| Db | 1784 | -ACGTGAGCCCCCAGAGTAAGAAAGTTTCAATTTGACCCCTTAACGAGAGATCCCAATGAG    | 1842 |
| Oy | 1774 | GCAATGGCGGAGTTTGGCAAGGAAATTTGACATCTCTGTGTCAAAATTTAGCAGGTGATC     | 1833 |
| Db | 1843 | GCCCTTCGAGAGTTCGCGCAAGGAGATTCGATGTCTCTGGGTCAAGATCGAGAGGTTGATTT   | 1902 |
| Oy | 1834 | GGACAGGGGAGATTGGCGAGGCTCTGACAGTGGCACCTCAACCTGCGACAGGCAAGAGAG     | 1893 |
| Db | 1903 | GGAGACTGGGAGATTTGGGGAAGTGTGCGGGGCTGGGCTTAAACTGCCCCGCGCGGGAG      | 1963 |
| Oy | 1894 | ATCTTTGTGGCATCAAGACGCTCAAGTGGGCTTACACGAGAGACAGCGCGGAGCTTTC       | 1953 |
| Db | 1963 | GTGTTCTGTGGCATCAAGACACTGAAGTGGGATACACGGAAGAGCAGCGGGGAGCTTTC      | 2022 |
| Oy | 1954 | CTGAGCGAAAGCTTCCATCATGTGGGCGAGTTTCGACATCTCCAAAGTCAATCAGTGGAGGT   | 2013 |
| Db | 2023 | CTGAGTAGGCTTCCATCATGTGGGTCAATTTTGAACCATCCAAATATATCTCGTCTAAGAGGCG | 2082 |

|   |      |  |      |
|---|------|--|------|
| Oy  | 2014 | GTCTGACCAAGAGACACACCTGGATGATCACCAGCAATTCATGTGGAATAGGCTCCCTG      | 2073 |
| Db  | 2083 | GTGGTCAACCAAAAGTGCCTCCAGTCATGATCTCTCAGTAATTATGAGAACTGTGCTCCTG    | 2142 |
| Oy  | 2074 | GACTCTCTTCTCCGGGCAAAAGATGGGACAGTTCCACAGTCATCCAGCTGGTGGCATGCTT    | 2133 |
| Db  | 2143 | GAGTCCTCCGACGGGCTCAATGACGGGGACAGTTCCAGAGTCATCCAGCTTGTGGCATGTGTG  | 2202 |
| Oy  | 2134 | CGGGGCATCCGAGCTGGCATGAAAGTACCTGGCAGACATGTAACCTATGTTCCACCCTG      | 2193 |
| Db  | 2203 | CGTGGCATTCCTGCGGACAGAAAGTACTTGTGTGAGATGACCTAGCTGCACCGTCACTTC     | 2262 |
| Oy  | 2194 | GCATCCCGCAAAATCCGTCGCAACACAGCAACCTGGTCTGCAAGTGTGGAGCTTTGGGGCTC   | 2253 |
| Db  | 2263 | GCTGCCCGCAACATCTTGTCAACAGCTACTTGGTCTGCAAAAGTATCTGACTTTGGGCTTC    | 2322 |
| Oy  | 2254 | TACAGCTTTCTAGAGACAGTATACCTCAGACCCACCTACACCAAGTGCCTGGGCGGAAG      | 2313 |
| Db  | 2323 | TCCGCGCTTCTGGAGAGACGACCCCTCAGACCCACTACACCAAGCTCCCTGGTGGGAAG      | 2382 |
| Oy  | 2314 | TTCCCATCCGCTGGACAGCCCCGGGAAGCCATTCAGTACCGGAAGTTCACCTCGGCCAGT     | 2373 |
| Db  | 2383 | ATCCCTATCCGTTGGACCGGCCACAGAGGCCATAGACTATCGGAAGTTCACAGCTCTCCAGC   | 2442 |
| Oy  | 2374 | GATGTGTGAGAGCTACGGGCATTTGTCATGTGGAGAGTATCTCTATGTGGGAGAGCGGCCATC  | 2433 |
| Db  | 2443 | GATGTGTGAGAGCTACGGGATCTGTCATGTGGAGAGTATAGGTACGAGAGGAGACATATC     | 2502 |
| Oy  | 2434 | TGGAGACATGACCAACACAGATGTATATCAATGCCATTGACAGACAGATATCGGCTGCCACCG  | 2493 |
| Db  | 2503 | TGGGACATGAGCAACCAAGATGTATCATATGCCGTAGACCAAGACTATCGGTTACCAACC     | 2562 |
| Oy  | 2494 | CCCATGAGACTGCCCCGAGCGCCCTGCACCAATCTATGCTGGAGTGTGGCAGAAAGACCGC    | 2553 |
| Db  | 2563 | CCCATGAGACTGCCAGCGGCGGCTGCACACAGCTATCTGACTGTGGGTGGCGGGAGCCGG     | 2622 |
| Oy  | 2554 | AACCAACGGGCCCCAAGTTCCGGCCAAATTTGTCAACAGCCTAGCAAAATGATCCGCAATCCC  | 2613 |
| Db  | 2623 | AACCTCAGGGCCCAAGTCTCCCAAAATCTGTCAACAGCCTAGCAAACTTATCCGCAAACTCT   | 2682 |
| Oy  | 2614 | AACAGCCTCAAAAGCATGGGGGCCCTCTCCTGTGGCATCAACCTGCGCGCTGTGGAGCCGC    | 2673 |
| Db  | 2683 | GCCAGCCTCAAGGTCAATCGCCAGTGGCCCATCTTGGCATCTCCAGGCCCTCTTAGACCCG    | 2742 |
| Oy  | 2674 | ACGATCCCGCATACACACAGCTTTAAACAGGTTGGAGAGTGGCTGGAGGCCATCAAGATG     | 2733 |
| Db  | 2743 | ACGGTCCCAAGTTATACAGACTTCAAGAGGAGTGGGAGCTGGCTAGATGCCATCAAGATG     | 2802 |
| Oy  | 2734 | GGGCGATGACAAAGAGAGCTTCCGCAATTCGCGGCTTCACTCCTTTGAGAGTGTGTCTAG     | 2793 |
| Db  | 2803 | GGGAGGTATAAAGAGACTTCTGTGGTGGGGGTTTTGCTCTCTTTGACCTGGTGGGCCGAG     | 2862 |
| Oy  | 2794 | ATGATGATGAGAGAGCATTTCTCCGGGTTGGGGTTCACTTTGGCTGGCCACCAAGAAAAATTC  | 2853 |
| Db  | 2863 | ATGAGCTSCAGAAAGTCTGCTAAAGATTCGGGGATCTATTGGCCGCGCACAGAAAGATTC     | 2922 |
| Oy  | 2854 | CTGAACAGTATCCAGGATGATGCGGGCGGAGATGAACCAATTCAGTCTGTGAGATTTTGA     | 2913 |
| Db  | 2923 | CTCAGCAATATCCAGGACATGGCGGTCTGACATGATACCAACAGCACTGCCGTGTGAGSTCTGA | 2982 |
| RESULT 14   |      |  |      |
| US-08-571-785-2   |      |  |      |
| Patent No. 5804411  |      |  |      |
| GENERAL INFORMATION:  |      |  |      |
| APPLICANT: KAJIMA, HISAO  |      |  |      |
| APPLICANT: KITAGAWA, KOICHIRO                                   |      |  |      |
| APPLICANT: OHNO, HIROYUKI                                       |      |  |      |
| APPLICANT: UENO, TOSHIO   |      |  |      |
| TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140 |      |  |      |
| TITLE OF INVENTION: AND DNAs encoding it                        |      |  |      |
| NUMBER OF SEQUENCES: 16   |      |  |      |

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RESULT 14
US-08-571-785-2
; Sequence 2, Application US/08571785
; Patent No. 5804411
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5804411a1 Polypeptide of Protein p140
; TITLE OF INVENTION: and DNAs encoding it
; NUMBER OF SEQUENCES: 16

```

Correspondence Address:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/571,785  
FILING DATE: 13-DEC-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/348,143  
FILING DATE: 23-NOV-1994  
APPLICATION NUMBER: JP 315806/1993  
FILING DATE: 24-NOV-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2982 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: skeletal muscle myoblast  
CELL LINE: L6  
US-08-571-785-2

Query Match 51.3%; Score 1520.8; DB 1; Length 2982;  
Best Local Similarity 71.7%; Pred. No. 0;  
Matches 2066; Conservative 0; Mismatches 772; Indels 42; Gaps 4;

52 GAGCTGGGCTGATGGTGCATCTCCATCAGGAGTGGGAAGAGTGGTACATGATGAG 111  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 127 GAGCTGGCATGATCATCTCATCCAGAGAGTGGTGGGAAGATGAGCGCTACGATGAA 166  
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QY 112 AACATGAACAGATCGCAGCATACAGGTGTGCAACGTGTTGATCAAGCAGAACAC 171  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 187 GCATGAATCTATCCGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 246  
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QY 172 TGGCTACGAGACCAATTTATCCGGGCGCGTGGGGCCACCCGATCCACGTTGAGATGAG 231  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 247 TGGCTCCGACCGCTTTCATCTGGCGGGAAGTCCAGCGCTTACGATGAGAGTGAAG 306  
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QY 232 TTTTCGCTGCTGACTGACAGCAGCATCCCGAGGCTGCTGCTGCTGCAAGAGACCTTC 291  
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Db 307 TTACCGTATGAGATGCAACAGCATCCCAACATCCCTGCTGCTGCAAGAGAACCTTC 366  
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QY 292 AACCTCTATATAGAGCTGACTTGTGCTGGCCACCAAGCCTTCCCAACTGGATG 351  
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Db 367 AACCTTTTACTACGAGCTGATAGCTGATGCTGAGCTGAGCTTCCTCTCTGATG 426  
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QY 352 GAGAAATCCATGGTGAAGTGGATACCATTTGACGCGGAGAGAGCTTCTCCAGGTGAG 411  
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Db 427 GAAAGCCCTACCTAGAAAGTGAACCATTTGCCAGATGAGAGCTTCTGCGAGTAGAC 486  
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QY 412 CTGGTGGCGCGCTCAVGAATCAACACAGAGTGGAGGCTTGGAGACTGTGCTCCGC 471  
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Db 487 GCTGGGCGC-----GTTAACACCAAGTGGCGAGCTTCCGCGCTTTCCAAA 534  
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QY 472 AGCGGCTTACCTGGCTCCAGAGCTATGGCGGCTGCACTGTCCCATCGCGCTGCGT 531  
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Db 535 GCGGCTTCTACTTATGCGCTTCCAGGACGAGGTGCTGATGTCATCTCTGTGCGC 594  
QY 532 GTCTTCTACCGCAATGTCCTCCCGCATCATCCAGATGCGGCATCTTCCAGAAACCTG 591  
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Db 595 GCTTCTACCAAGAAATGTGATCCACACCTGACGCTTCCACACTCTCCCGAGACCTC 654  
QY 592 TCGGGGGCTAGAGACATAGCTGCTGGTGGTGGCGGGGCGACAGCTGACCAATGCGGAA 651  
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Db 655 ACGGGGCTAGCCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714  
QY 652 GAGGTGATGTACCATCAAGCTCTACTGTACGAGGAGCGGAGAGTGGTGGCCATC 711  
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Db 715 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774  
QY 712 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771  
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Db 775 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834  
QY 772 TGTTCATCTGGACCTTTCAGGCAACCAAGGAGTGGCTGTACCCACTGTCCATC 831  
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Db 835 TGTCCCTGCGAGCTTACAAAGCAAGAGAGAGGCGCTGCTGCTGCTGCTGCTGCTG 894  
QY 832 AACAGCGGACCACTTCTGAAGGGGCCACCACTGTGTGCTGCGCAATGCTACTACAG 891  
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Db 895 AATAGCGGACCACTTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 954  
QY 892 GCAAGCTGAGCCCTGCGGATGCTGCGGCAACCACTGCTGCTGCTGCTGCTGCTG 951  
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Db 955 GCAAGCTGAGCCCTGCGGATGCTGCGGCAACCACTGCTGCTGCTGCTGCTGCTG 1014  
QY 952 ATTTCAGTCAATGAGACCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011  
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Db 1015 ATCTCAGTGTGATGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074  
QY 1012 GCGCGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056  
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Db 1075 GGAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134  
QY 1057 TCGGGCGGGGGTGGCTGCGGATGCTGCGGAGCAATGATGATGATGATGATGATG 1116  
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Db 1135 GAGAGTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194  
QY 1117 GGCCTGACGAGCCACGATTTACATGATGATGATGATGATGATGATGATGATGATG 1176  
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Db 1195 GGCCTGACGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254  
QY 1177 GAGATCAGGCTGTGAAGCGGCTTACTGACCAAGGCCCTTCTGCTGCTGCTGCTG 1236  
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Db 1255 GAGGTGAGGCTGTGAAGCGGCTTCTGCGGCAAGAGCCCTTGGCGGCTGCTGCA 1314  
QY 1237 GTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1296  
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Db 1315 GTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1374  
QY 1297 GCGACGCTGAGACATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1356  
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Db 1375 AGTTCAGGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434  
QY 1357 CTGACTATGAGCTGAGTCTATGAGAGGAGCTCAGTGAATGATGATGATGATGATG 1416  
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Db 1435 TTGAGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1494  
QY 1417 AAAAGCCCCACCAATACGGCTACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1476  
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Db 1495 CAGAAAGACTCTGATCAACTGAGAGGCTGAGAGGCGGAGCGGCTGATGATGATGATG 1554  
QY 1477 CCGGAGCGACTGTGAGAGGCTGAGGCGCTGAGAGGCGGCAAGATGATGATGATGATG 1536  
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Db 1555 CCGGCTGCGACATGATGAGAGTGTAGGAGATGATGATGATGATGATGATGATGATG 1614  
QY 1537 ACAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1593  
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Db 1615 AGTGAAGAGGCTGAGAGGCGGCGAGAGCTTCAAGAGAGCTTCCCTAATGTTGGATCC 1674

|    |      |  |      |
|----|------|--|------|
| Oy | 1594 | TGGCCGCTGGCCGCTGCTCTTCTCTCAATTCCTGTGGTTGTCAATGCCAATCTGTGTAAACA   | 1653 |
| Db | 1675 | ACCGTAGCTGGCTTTGCTTTCTATGCTGGTGTCTCTGTGGCATTTGCTTTGCTCTCCCTGAG   | 1734 |
| Oy | 1654 | CGGGGATTGTGAGCGTGTGCTGACTCTCGAGTACACGGACAAGCTGGCAACACTACACAGTGGC | 1713 |
| Db | 1735 | AAGCAGGCCCAAGGGGCCCTGATGTCAGAAATACACGGAGAACTTGCAGCAAT-----       | 1783 |
| Oy | 1714 | CACATTAACCCAGCAGCATGAAATCTACATGCATCTTTACCTACCTACGAGACCCCAACGAG   | 1773 |
| Db | 1784 | -ACGTTGGCCCCAGAGATGAAAGTTTACATTGACCCCTTTACCTACGAGAGATCCCAATGAG   | 1842 |
| Oy | 1774 | GCACTGGGGGAGTTTGGCAAGGAAATTGAACTCCCTGTGTGCAAAATTGAGACAGTATC      | 1833 |
| Db | 1843 | GCCTTCGAGAGTTTCCGCAAGAGATGATGTGTCTGTGGCAAGATCTGAGAGAGTATTT       | 1902 |
| Oy | 1834 | GGACACAGGGAGTTTGGCGAGGCTCTGCAGTGGCCACCTGGAAGCTGCCAGCAAGAGAGAG    | 1893 |
| Db | 1903 | GGACCTGGGGAGTTTGGGGAAGTGTGCCGGGGTGGCTGAACACTGCCCGCCCGGGGAG       | 1962 |
| Oy | 1894 | ATCTTTTGGCCATTCAGAGCGCTTCAGTCTGGGCTACACGGAGAAACAGCCCGGAGATTCT    | 1953 |
| Db | 1963 | GTTGTTCTGGCCATTCAGACACTGTGAAGTGGATATACCGAGAGCGACGCGCGGACTTC      | 2022 |
| Oy | 1954 | CTGAGCGAACCCTTCATCATATGAGGCCAGTTGTGACATCTCCAAAGCTCATCACTGGAGGGT  | 2013 |
| Db | 2023 | CTGAGTAGAGCTTTCATCATAGGGTCAATTGACATCCAAATTAATCCGCTTAGAGGGC       | 2082 |
| Oy | 2014 | GTCGTACCAAGACACACTCTGTGATGATCATACCGAGTTCAATGGAATGGCTCCCTG        | 2073 |
| Db | 2083 | GTTGTATCTTCAAAAGTGTCTCAGTCAATGATCTCTCACTGAGTTCAATGAGAACTGTGCCCTG | 2142 |
| Oy | 2074 | GACTCTTTTCTCCGGCAAAACATGAGGCAAGTACACAGTATCCAGCGGGGGGCAATGCTT     | 2133 |
| Db | 2143 | GACTCTTCTCTACGGCTCAATGACGGCACTTACAGTCACTCCAGCTTGTGGGCAATGTTG     | 2202 |
| Oy | 2134 | CGGGGCAATGCACTGGCATGAAAGTACTGTGGCAGACATGAATGTTGACCCGTGACCTG      | 2193 |
| Db | 2203 | CGTGGCAATGTCTCCGGCATGAAGTACTGTCTGTGAGATGAACTACGTGACCGGTGACCTC    | 2262 |
| Oy | 2194 | GCATCCCGCAACATCTCTGTCACACACACACCTGTGTGCAAGGTCTCGGACTTTGGGCTC     | 2253 |
| Db | 2263 | GCATCCCGCAACATCTCTGTCACACACACATCTGTGTGCAAGTACTACATTTGGGCTC       | 2322 |
| Oy | 2254 | TCACGCTTTCTAGAGAGCATACCTTCAGACCCCACTTACACCAAGTCCCTGGGCGGAAG      | 2313 |
| Db | 2323 | TCACGCTTTCTAGAGAGCATACCTTCAGACCCCACTTACACCAAGTCCCTGGGCGGAAG      | 2382 |
| Oy | 2314 | TTTCCCATCTCGGCGGACACCCCGGAAAGCATTCAGTACCGBAAGTTCACTCTGGCCACT     | 2373 |
| Db | 2383 | ATTCCTATCTGTTGGACCCCGCAGAGGCAATGACTTATCGGAAGTCCAGCTCTGCAAC       | 2442 |
| Oy | 2374 | GATGTGTGAGGCTACGGCAATTTGTCAATGTGGAGGTGATCTCTATGGCAGAGGGCCCTAC    | 2433 |
| Db | 2443 | GATGTGTGAGGCTACGGGATTCGTCAATGTGGAGGTGATGAGTACGAGAGGACACATAC      | 2502 |
| Oy | 2434 | TGGGACATGACCAACCAAGATATTAATCAATGCCATTGAGCAGAGACTATTCGCTGCCACCG   | 2493 |
| Db | 2503 | TGGGACATGAGCAACCAAGATATTAATCAATGCGGTAGAGCAAGACTATTCGCTTACACCC    | 2562 |
| Oy | 2494 | CCCATGTGACTGCCGAGCGCCCTGTGACCAACATCATGTGGAGACTGTTGGAGAAAGAGACGC  | 2553 |
| Db | 2563 | CCCATGTGACTGCCAGCGCGCTGTGACCAACGCTCATGTGTGACTGTTGGGTGCGGAGACGG   | 2622 |
| Oy | 2554 | AACCAACGGGCCCAATGTTGGCCAAATTTGTCAACACGCTAGACAAAGATGATCGCAATCC    | 2613 |
| Db | 2623 | AACCTAGAGCCCAATGTTTCCCAATTCGTCAACAGCTAGACAAACCTTATCCGCAATGCT     | 2682 |
| Oy | 2614 | AACACCTTCAAAAGCATGGGCGCCCTCTCTCTCTGACATCAACCTGGCGCTGTGACCGC      | 2673 |
| Db | 2683 | GCCACGCTCAAGGTATATGCCAGTGTCCCATCTGTGCAATGTCCCAACCCCTCTCTTAACCGC  | 2742 |

|    |      |  |       |
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| Qy | 2674 | ACGATCCCCGACTACACAGCTTTAAACAGCGTGGAGAGGCGTGGAGCCATCAAGT        | 27333 |
| Db | 2743 | ACGGTCCCAAGTTTACGACCTTCACGACCGGTGGCGACTGGCTGATGATCCATCAAGTT    | 28020 |
| Qy | 2734 | GGCGAGTACANGAGAGCTTGGCCAAATGCCCGCTTCACCTCTTGTGACGTCGTCTAG      | 27933 |
| Db | 2803 | GGGAGGTTTAAAGAGACCTTCGTGGGCGGGTTTTGGCTCCTTTGACCTGGTGGCCAG      | 28632 |
| Qy | 2794 | ATGATGATGGAGGACATTCCTCCGGGTTGGGGTACCTTTGGCTGGCCACACAGAAAAATC   | 28533 |
| Db | 2863 | ATGACTGCAGAAAGTCTGCTPAAGATTCGGGGTCACTTTGGCCGGCACACAGAAAGATC    | 29222 |
| Qy | 2854 | CTGAACAGTATCCAGTGTATGGCGGGCGGAGATGAACAGATTCACTGTGTGAGATTTGA    | 29133 |
| Db | 2923 | CTCAGCAAGTATCCAGGACATGGCGGCTGCGAGATGAACCAACACTCCCGTGCAGGTTCTGA | 29892 |

RESULT 15  
US-08-162-809-1

; Sequence 1, Application US/08162809  
: Patent No. 5457049

GENERAL INFORMATION:

APPLICANT: pasquale, Elena B

TITLE OF INVENTION: NOVEL EPH-RE

| TITLE OF INVENTION:  | NUCLEOTIDE SEQUENCES, AND METHODS OF USE |
|----------------------|--|
| NUMBER OF SEQUENCES: | 36                                       |

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Tijera Village Blvd - 700

CITY: San Diego

STATE: California  
COUNTRY: United States of America

ZIP: 92122

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; COMPUTER READABLE FORM:
MEDIUM TYPE: E13000 4151

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COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS
SOFTWARE: Patent To Police

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CURRENT APPLICATION DATA: 4.0 / VERSION #1.23

APPLICATION NUMBER: US/08/162,809

CLASSIFICATION: 514

NAME: Campbell Cathryn

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 950

TELEPHONE: (619) 535-9000

TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO. 1

SEQUENCE CHARACTERISTICS:

LENGTH: 3133 base pairs  
TYPE: nucleic acid

; STRANDEDNESS: both

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POLYLOG: linear
FEATURE:

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| NAME/KEY: | CDS |
|-----------|-----|
|-----------|-----|

LOCALION: JOHN(3..419, 421..2858)  
US-08-162-809-1

Query Match      A9 68:    Score 1460 6:    DB 1:    Length 3333

Best Local Similarity 70.78; Pred. No. 0;

matches 2096; conservative 0; Mismatches 704; Indels 164; Gaps 4;

18 AGAACGCTATGGACTCCACTACAGCGACTGCTGAGCTGGGCTGGATGGTGATCCCTCC 77

[illegible][illegible]

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198 CCGTGGGGCCACCGACCTGACGATGAAGTTTGGGTGCGGACTGCGACGACAT 257  
182 GCGCGAGCGCCACCGACCTGACGATGAAGTTTGGGTGCGGACTGCGACGACAT 241  
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